

GenCore version 5.1.6
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in search, using sw model

ril 2, 2004, 10:11:59 ; Search time 54 Seconds
(without alignments)
612.186 Million cell updates/sec

-10-066-273-9

9
MIVFGWAVLASRLGQGLL.....QNVDELVDLTAVIRTLVDK 117

OSUM62

pop 10.0 , Gapext 0.5

86107 seqs, 282547505 residues

ts satisfying chosen parameters: 1586107

gth: 0

gth: 2000000000

inimum Match 0%

aximum Match 100%

isting first 45 summaries

_Geneseq_29Jan04:*

Geneseqp1980s:*

Geneseqp1990s:*

Geneseqp2000s:*

Geneseqp2001s:*

Geneseqp2002s:*

Geneseqp2003as:*

Geneseqp2003bs:*

Geneseqp2004s:*

the number of results predicted by chance to have a
r than or equal to the score of the result being printed,
ed by analysis of the total score distribution.

SUMMARIES

ery	rch	Length	DB	ID	Description
0.0	0.0	117	4	AAB31180	Amino aci
0.0	0.0	117	6	ABO25151	Novel hum
0.0	0.0	117	6	ABU67269	Novel hum
0.0	0.0	117	6	ABU72037	Novel hum
0.0	0.0	117	6	ABU67138	Novel hum
0.0	0.0	117	6	ABU79780	Human sec
0.0	0.0	117	6	ABO33583	Novel hum
0.0	0.0	117	6	ADA47181	Human sec
0.0	0.0	117	7	ABO44436	Human sec
0.0	0.0	117	7	ABO33460	Novel hum
0.0	0.0	117	7	ABO19838	Human sec
0.0	0.0	117	7	ADC17875	Human PRO
0.0	0.0	117	7	ADD10295	Human sec
0.0	0.0	117	7	ADD11255	Human sec
0.0	0.0	117	7	ADD70521	Human sec
0.0	0.0	117	7	ADD39598	Human sec
0.0	0.0	117	7	ADD70044	Human sec
0.0	0.0	117	7	ADD37048	Human sec
0.0	0.0	117	7	ADD38165	Human sec
0.0	0.0	117	7	ADD39121	Human sec
0.0	0.0	117	7	ADD38644	Human sec
0.0	0.0	117	7	ADD40075	Human sec
0.0	0.0	117	7	ADE50296	Human sec
0.0	0.0	117	7	ADE19908	Human sec
0.0	0.0	117	7	ADE49819	Human sec

26	609	100.0	117	7	ADE21377	H
27	609	100.0	117	8	ADE41256	H
28	609	100.0	117	8	ADE41104	H
29	609	100.0	118	3	AAV99341	H
30	609	100.0	118	4	AAB66090	P
31	609	100.0	118	5	ABB84819	H
32	609	100.0	118	5	ABB95425	H
33	604	99.2	289	4	AAM25871	H
34	604	99.2	427	2	AAV25761	H
35	604	99.2	427	3	AAB32412	H
36	604	99.2	436	3	AAB32411	H
37	604	99.2	576	3	AAB32384	H
38	604	99.2	576	4	AAB94297	H
39	604	99.2	576	5	ABP64699	H
40	85	14.0	961	6	ABU21450	P
41	79.5	13.1	5002	4	ABB63723	D
42	78	12.8	1527	2	AAW81172	H
43	78	12.8	1531	2	AAW81173	H
44	77	12.6	2618	4	ABG02135	N
45	77	12.6	2622	4	ABG06418	N

ALIGNMENTS

RESULT 1

AAB31180
ID AAB31180 standard; protein; 117 AA.

AC AAB31180;

DT 20-APR-2001 (first entry)

DE Amino acid sequence of human polypeptide PRO444.

XX Human; secreted protein; transmembrane protein; PRO186; PRO444; I
KW PRO185; PRO210; PRO215; PRO217; PRO242; PRO288; PRO365; PRO1361;
KW PRO1183; PRO1272; PRO1419; PRO4999; PRO7170; PRO248; PRO353; PRO1
KW PRO1600; PRO3940; PRO533; PRO301; PRO187; PRO1411; PRO43E
KW PRO246; PRO265; PRO941; PRO10096; PRO6003; PRO6004; PRO350; PRO26
KW PRO6309; cell death; genetic disorder; transgenic animal; gene tr
XX Homo sapiens.

Key	Location/Qualifiers
Peptide	1..16
Modified-site	/note= "signal peptide"
Modified-site	18..24
Modified-site	/note= "N-myristoylation site"
Modified-site	32..38
Modified-site	/note= "N-myristoylation site"
Modified-site	34..40
Modified-site	/note= "N-myristoylation site"
Modified-site	35..41
Modified-site	/note= "N-myristoylation site"
Modified-site	51..57
Modified-site	/note= "N-myristoylation site"

WO200077037-A2.

21-DEC-2000.

22-MAY-2000; 2000WO-US014042.

15-JUN-1999; 99US-0139695P.
20-JUL-1999; 99US-0145070P.
26-JUL-1999; 99US-0145698P.
17-AUG-1999; 99US-0149396P.
01-SEP-1999; 99WO-US020111.
08-SEP-1999; 99WO-US020594.
15-SEP-1999; 99WO-US021090.
15-SEP-1999; 99WO-US021547.
30-NOV-1999; 99WO-US028313.

99WO-US028301.
 99WO-US028565.
 99US-0169495P.
 2000WO-US000219.
 2000WO-US000431.
 2000WO-US000432.
 2000WO-US000414.
 2000WO-US0005601.
 2000WO-US0005841.
 2000WO-US0007377.
 2000WO-US0008439.
 2000WO-US013358.
 2000WO-US013705.
 VTECH INC.
 Baker KP, Botstein DA, Desnovers L, Eaton DL;
 Gong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
 Gurney AL, Kijavini LJ, Mather JP, Napier MA, Pan J;
 Py MA, Stewart TA, Tumas D, Watanabe CK, Williams PM;
 Yang Z;
 091/06.
 5965.
 leic acid molecule encoding a PRO polypeptide which is a
 polypeptide is useful for gene therapy and identification
 polypeptides.
 J 4; 244pp; English.
 sequence represents a human secreted and transmembrane
 The specification describes human polypeptides, designated
 14, PRO183, PRO185, PRO210, PRO215, PRO217, PRO242, PRO288,
 61, PRO1308, PRO1183, PRO1272, PRO1419, PRO4999, PRO7170,
 53, PRO1318, PRO1600, PRO9940, PRO5133, PRO301, PRO187,
 11, PRO4356, PRO245, PRO365, PRO941, PRO10096, PRO6003,
 150, PRO2630 and PRO6309. The biological activity of cells
 ited with agents that bind to these polypeptides, resulting
 of the cells. The polynucleotides encoding these
 are useful in the recombinant production of the
 as a hybridisation probe to screen libraries to isolate
 sequences, or to map the gene. They may also be used for
 etic disorders, and to produce transgenic animals which are
 le development and screening of therapeutically useful
 e polynucleotides can also be used in gene therapy e.g. to
 ictive gene
 AA;
 100.0%; Score 609; DB 4; Length 117;
 arity 100.0%; Pred. No. 2e-63;
 conservative 0; Mismatches 0; Indels 0; Gaps 0;
 GWAVFLASRLGQGLLLTLEERHIAFLPTGGATTMGNSICRDSDGDDSDVDTQQ 60
 GWAVFLASRLGQGLLLTLEERHIAFLPTGGATTMGNSICRDSDGDDSDVDTQQ 60
 ENSAVPTADTRSPQDPVPPRRGRGPHPEPRKKQNVGVLDTLAVIRLVNDK 117
 ENSAVPTADTRSPQDPVPPRRGRGPHPEPRKKQNVGVLDTLAVIRLVNDK 117
 idard; protein; 117 AA.
 (first entry)
 secreted and transmembrane protein PRO444.

KW Human; secreted and transmembrane protein; PRO; antidiabetic;
 KW ophthalmological; cytostatic; immunostimulant; gene therapy;
 KW vascular endothelial growth factor inhibitor; hypertrophy of adu
 KW protein secretion disorder; pancreas disorder; diabetes;
 KW vascular permeability; retinal neuron cell survival; retinal dis
 KW immune response; inflammation; mononuclear cell infiltration;
 KW eosinophil infiltration; apoptosis; neoplastic growth.
 XX Homo sapiens.
 XX
 XX US2003040014-A1.
 XX
 XX 27-FEB-2003.
 XX
 XX 01-FEB-2002; 2002US-00066269.
 XX
 XX 26-AUG-1997; 97US-0056974P.
 XX 17-SEP-1997; 97US-0059115P.
 XX 18-SEP-1997; 97US-0059263P.
 XX 19-SEP-1997; 97US-0059588P.
 XX 17-OCT-1997; 97US-0062285P.
 XX 24-OCT-1997; 97US-0062816P.
 XX 24-OCT-1997; 97US-0063082P.
 XX 27-OCT-1997; 97US-0063329P.
 XX 29-OCT-1997; 97US-0063733P.
 XX 21-NOV-1997; 97US-0066364P.
 XX 25-NOV-1997; 97US-0066840P.
 XX 16-DEC-1997; 97US-0069694P.
 XX 09-FEB-1998; 98US-0074086P.
 XX 09-FEB-1998; 98US-0074092P.
 XX 25-MAR-1998; 98US-0075294P.
 XX 08-APR-1998; 98US-0081049P.
 XX 14-JUL-1998; 98WO-US014552.
 XX 10-AUG-1998; 98US-0095988P.
 XX 18-AUG-1998; 98US-0097000P.
 XX 09-SEP-1998; 98US-0099601P.
 XX 10-SEP-1998; 98US-0099803P.
 XX 10-SEP-1998; 98US-0099812P.
 XX 10-SEP-1998; 98US-0099812P.
 XX 14-SEP-1998; 98WO-US018824.
 XX 16-SEP-1998; 98WO-US019093.
 XX 16-SEP-1998; 98WO-US019330.
 XX 17-SEP-1998; 98US-0100858P.
 XX 17-SEP-1998; 98WO-US019437.
 XX 24-SEP-1998; 98US-0101922P.
 XX 28-OCT-1998; 98US-0106032P.
 XX 20-NOV-1998; 98US-0109304P.
 XX 20-NOV-1998; 98WO-US024855.
 XX 25-NOV-1998; 98WO-US025130.
 XX 01-DEC-1998; 98WO-US025108.
 XX 08-MAR-1999; 99WO-US005028.
 XX 23-MAR-1999; 99US-0125778P.
 XX 02-JUN-1999; 99WO-US012252.
 XX 15-JUN-1999; 99US-0139695P.
 XX 20-JUL-1999; 99US-0145070P.
 XX 26-JUL-1999; 99US-0145698P.
 XX 17-AUG-1999; 99US-0149396P.
 XX 01-SEP-1999; 99WO-US020111.
 XX 08-SEP-1999; 99WO-US020594.
 XX 15-SEP-1999; 99WO-US021090.
 XX 30-NOV-1999; 99WO-US021547.
 XX 01-DEC-1999; 99WO-US028313.
 XX 02-DEC-1999; 99WO-US028301.
 XX 07-DEC-1999; 99US-0169495P.
 XX 20-DEC-1999; 99WO-US030999.
 XX 05-JAN-2000; 2000WO-US000219.
 XX 18-FEB-2000; 2000WO-US004341.
 XX 22-FEB-2000; 2000WO-US004342.
 XX 01-MAR-2000; 2000WO-US004414.
 XX 02-MAR-2000; 2000WO-US005601.
 XX 09-MAR-2000; 2000WO-US005841.
 XX 09-MAR-2000; 2000WO-US006471.

?GWAFLASRLGQGLLLTLEEHIAHFLGTGGAATTMGNSICRDDSGTDDSDVDTQ 60
 ?GWAFLASRLGQGLLLTLEEHIAHFLGTGGAATTMGNSICRDDSGTDDSDVDTQ 60
 ?GWAFLASRLGQGLLLTLEEHIAHFLGTGGAATTMGNSICRDDSGTDDSDVDTQ 60

17-AUG-1999; 99US-0149396P;

99WO-US020111.
 99WO-US020594.
 99WO-US021090.
 99WO-US021547.
 99WO-US028313.
 99WO-US028301.
 99WO-US028565.
 99US-0169495P.
 99WO-US030999.
 2000WO-US000219.
 2000WO-US004341.
 2000WO-US004342.
 2000WO-US004414.
 2000WO-US005601.
 2000WO-US005841.
 2000WO-US006471.
 2000WO-US007377.
 2000WO-US008439.
 2000WO-US013358.
 2000WO-US013705.
 2000WO-US014042.
 2000WO-US014941.
 2000WO-US015264.
 2000WO-US02031.
 2000WO-US023522.
 2000WO-US023328.
 2000WO-US032678.
 2001WO-US006520.
 2001WO-US017443.
 2001WO-US017800.
 2001WO-US019692.
 2001WO-US021066.
 2001WO-US021735.
 2001US-00002796.

TECH INC.

Baker KP, Botstein DA, Desnoyers L, Eaton DL, Gurney AL, Kljavin IJ, Mather JP, Napier MA, Pan J, Y MA, Stewart TA, Tumas D, Watanabe CK, Williams PM; 482/31.
 455.

d and transmembrane polypeptide for modulating biological cell expressing the polypeptide, for identifying agonists or f polypeptide, and as molecular weight markers.

4; 254pp; English.

describes an isolated, secreted and transmembrane PP), termed PRO PP or fibroblast growth factor receptor PP useful for detecting PRO333, PRO301, PRO187, PRO337, PRO1411, 246, PRO6307, PRO6003, fibroblast growth factor receptor R-4, FGFR-1, FGFR-2, PRO6004, PRO4356, PRO2630, PRO265 or ptide, and for linking a bioactive molecule to a cell e above polypeptides. The bioactive molecule, a toxin, an antibody, causes cell death. PRO is useful in assays to r proteins or molecules involved in binding interaction. The e (ii) encoding (i) is useful in chromosome and gene eneration of antisense RNA and DNA, for generating imals or knockout animals which in turn are useful in the nd screening of therapeutically useful reagents, to ridisation probes for mapping the gene which encodes the PRO enetic analysis of individuals with genetic disorders, in for chromosome identification and as a chromosome marker. are useful for tissue typing. This is the amino acid novel human secreted and transmembrane PRO polypeptide

AA;

Query Match 100.0%; Score 609; DB 6; Length 117;
 Best Local Similarity 100.0%; Pred No. 2e-63;
 Matches 117; Conservative 0; Mismatches 0; Indels 0; C

QY 1 MIVFGWAVFLASRLSGQLLLTLBEHIAHFLGTGAATTMGNSICRDDSCTDDSV
 Db 1 MIVFGWAVFLASRLSGQLLLTLBEHIAHFLGTGAATTMGNSICRDDSCTDDSV
 QY 61 QQAENSAPVTADTRSPQRPDPVPRRGPGPHEPRKKQNVGLVLDLTLAVIRTLVI
 Db 61 QQAENSAPVTADTRSPQRPDPVPRRGPGPHEPRKKQNVGLVLDLTLAVIRTLVI

RESULT 5
 ABU67138
 ID ABU67138 standard; protein; 117 AA.
 XX
 AC ABU67138;
 XX
 DT 28-MAY-2003 (first entry)
 XX
 DE Novel human secreted and transmembrane protein PRO444.
 XX
 KW Secreted and transmembrane polypeptide; PRO polypeptide; PRO533;
 KW PRO187; PRO337; PRO1411; PRO10096; PRO246; PRO6307; PRO6003; PRO
 KW PRO4356; PRO2630; PRO265; PRO941; FGFR; bioactive molecule;
 KW fibroblast growth factor receptor; cell death; chromosome mapping
 KW gene mapping; transgenic animal; knockout animal; gene therapy; i
 KW obesity; diabetes; insulinaemia; vascular permeability;
 KW cardiac insufficiency disorder; immune response; hearing loss;
 KW auditory hair cell regeneration; bone disorder; cartilage disorde
 KW sports injury; arthritis.
 XX
 OS Homo sapiens.
 XX
 FN US2003032062-A1.
 XX
 PD 13-FEB-2003.
 XX
 PF 01-FEB-2002; 2002US-00066273.
 XX
 PR 26-AUG-1997; 97US-0056974P.
 PR 17-SEP-1997; 97US-0059115P.
 PR 18-SEP-1997; 97US-0059263P.
 PR 19-SEP-1997; 97US-0059588P.
 PR 17-OCT-1997; 97US-0082285P.
 PR 24-OCT-1997; 97US-0062816P.
 PR 24-OCT-1997; 97US-0063082P.
 PR 27-OCT-1997; 97US-0063329P.
 PR 29-OCT-1997; 97US-0063733P.
 PR 21-NOV-1997; 97US-0066364P.
 PR 25-NOV-1997; 97US-0066840P.
 PR 16-DEC-1997; 97US-0069694P.
 PR 09-FEB-1998; 98US-0074086P.
 PR 09-FEB-1998; 98US-0074092P.
 PR 25-MAR-1998; 98US-0079294P.
 PR 08-APR-1998; 98US-0081049P.
 PR 14-JUL-1998; 98WO-US014552.
 PR 10-AUG-1998; 98US-0095938P.
 PR 18-AUG-1998; 98US-0097000P.
 PR 09-SEP-1998; 98US-0099601P.
 PR 10-SEP-1998; 98US-0099803P.
 PR 10-SEP-1998; 98US-0099811P.
 PR 10-SEP-1998; 98US-0099812P.
 PR 14-SEP-1998; 98WO-US018824.
 PR 16-SEP-1998; 98WO-US019093.
 PR 17-SEP-1998; 98WO-US019330.
 PR 17-SEP-1998; 98US-0100858P.
 PR 17-SEP-1998; 98WO-US019437.
 PR 24-SEP-1998; 98US-0101922P.
 PR 28-OCT-1998; 98US-0106032P.
 PR 20-NOV-1998; 98US-0109304P.
 PR 20-NOV-1998; 98WO-US024855.

98WO-US025190.
98WO-US025108.
98WO-US005028.
99US-0125778P.
99WO-US012252.
99US-0139695P.
99US-0145070P.
99US-0145698P.
99US-0149396P.
99WO-US020111.
99WO-US020594.
99WO-US021090.
99WO-US021547.
99WO-US028313.
99WO-US028301.
99WO-US028565.
99US-0169495P.
99WO-US030999.
2000WO-US000219.
2000WO-US004341.
2000WO-US004342.
2000WO-US004414.
2000WO-US005601.
2000WO-US005841.
2000WO-US006471.
2000WO-US007377.
2000WO-US008439.
2000WO-US013358.
2000WO-US013705.
2000WO-US014042.
2000WO-US014941.
2000WO-US015264.
2000WO-US022031.
2000WO-US023522.
2000WO-US023328.
2000WO-US032678.
2001WO-US006520.
2001WO-US017443.
2001WO-US017800.
2001WO-US019692.
2001WO-US021066.
2001WO-US021735.
2001US-00002796.

NTECH INC.

, Baker KP, Botstein DA, Deenoyers L, Eaton DL,
Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A,
Gurney AL, Klijavin IJ, Mather JP, Napier MA, Pan J,
oy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM,
ang Z;

1963/32.
4445.

and transmembrane polypeptide for modulating biological
a cell expressing the polypeptide, identifying agonists or
of the polypeptide, and as molecular weight markers.

3 4: 254pp; English.

n describes an isolated, secreted and transmembrane
(I), termed PRO polypeptide. (I) is useful for detecting
01, PRO187, PRO337, PRO1411, PRO10096, PRO246, PRO6307,
6004, PRO4356, PRO2630, PRO265, PRO941, fibroblast growth
toxin (FGFR)-4, FGFR-2 or FGFR-1 polypeptide, and for
oactive molecule e.g. toxin, radiolabel or antibody, to a
ing the polypeptides. The bioactive molecule causes cell
is useful as hybridisation probes, in chromosome and gene
generation of antisense RNA and DNA, in the preparation of
ide, for generating transgenic animals or knockout animals
n are useful in the development and screening of
lly useful reagents, and for the genetic analysis of

CC individuals with genetic disorders, in gene therapy, and for chr
identification. (I) Or Ab is useful for the preparation of medic
CC treating conditions which are responsive to the PRO polypeptide
CC PRO antibody e.g. a tumour. (I) is useful for treating obesity,
CC or hypo- or hyper-insulinaemia, and cardiac insufficiency disord
CC inhibiting tumour growth, enhances vascular permeability and imm
CC response, for inducing regeneration of auditory hair cells and f
CC treating hearing loss in mammals, and for treating bone and/or c
CC disorders such as sports injuries and arthritis. This is the ami
CC sequence of a novel human secreted and transmembrane polypeptide
XX
SQ

Sequence 117 AA;

Query Match 100.0%; Score 609; DB 6; Length 117;
Best Local Similarity 100.0%; Pred. No. 2e-63;
Matches 117; Conservative 0; Mismatches 0; Indels 0;

QY 1 MIVFGWAVFLASRLSGGGLLTLEEHIAHFLGTGGATTMGNSICRDSGTDD
Db 1 MIVFGWAVFLASRLSGGGLLTLEEHIAHFLGTGGATTMGNSICRDSGTDD
QY 61 QQAENSAVPTADTRSQPRDPVPRPRGRGPHEPRKKQNVGLVLTAVIRTLV
Db 61 QQAENSAVPTADTRSQPRDPVPRPRGRGPHEPRKKQNVGLVLTAVIRTLV

RESULT 6

ABU79780
ID ABU79780 standard; protein; 117 AA.
XX AC ABU79780;
XX DT 19-JUN-2003 (first entry)
XX DE Human secreted/transmembrane protein PRO444.
XX KW Human; secreted protein; transmembrane protein; PRO; genetic dis
XX OS gene therapy.
XX OS Homo sapiens.
PN US2003032057-A1.
XX PD 13-FEB-2003.
XX PF 15-NOV-2001; 2001US-00002796.
XX PR 26-AUG-1997; 97US-0056974P.
PR 17-SEP-1997; 97US-0059115P.
PR 18-SEP-1997; 97US-0059263P.
PR 19-SEP-1997; 97US-0059588P.
PR 17-OCT-1997; 97US-0062285P.
PR 24-OCT-1997; 97US-0062816P.
PR 24-OCT-1997; 97US-0063082P.
PR 27-OCT-1997; 97US-0063329P.
PR 29-OCT-1997; 97US-0063733P.
PR 21-NOV-1997; 97US-0066364P.
PR 25-NOV-1997; 97US-0066840P.
PR 16-DEC-1997; 97US-0069694P.
PR 09-FEB-1998; 98US-0074086P.
PR 09-FEB-1998; 98US-0074092P.
PR 25-MAR-1998; 98US-0079294P.
PR 08-APR-1998; 98US-0081049P.
PR 14-JUL-1998; 98WO-US014552.
PR 10-AUG-1998; 98US-0095998P.
PR 18-AUG-1998; 98US-0097000P.
PR 09-SEP-1998; 98US-0098601P.
PR 10-SEP-1998; 98US-0099803P.
PR 10-SEP-1998; 98US-0099811P.
PR 10-SEP-1998; 98US-0099812P.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019093.
PR 16-SEP-1998; 98WO-US019330.

relates to an isolated, secreted/transmembrane polypeptide, typeptide, having at least 80% sequence identity to a sequence encoded by one of the 37 sequences appearing as ABU9779 to a sequence encoded by a nucleic acid molecule deposited to the ATCC numbers given in the specification. Also included is a secreted/transmembrane polypeptide having at least 80% identity to a sequence selected from any one of the 37 cDNA

XX

2001US-00015869.
PR 08-OCT-1998; 98US-0103633P.
PR 08-OCT-1998; 98US-0103678P.
PR 08-OCT-1998; 98US-0103679P.
PR 08-OCT-1998; 98US-0103711P.
PR 14-OCT-1998; 98US-0104257P.
PR 20-OCT-1998; 98US-0104987P.
PR 20-OCT-1998; 98US-0105000P.
PR 20-OCT-1998; 98US-0105002P.
PR 21-OCT-1998; 98US-0105104P.
PR 22-OCT-1998; 98US-0105169P.
PR 22-OCT-1998; 98US-0105266P.
PR 26-OCT-1998; 98US-0105693P.
PR 26-OCT-1998; 98US-0105694P.
PR 27-OCT-1998; 98US-0105807P.
PR 27-OCT-1998; 98US-0105881P.
PR 27-OCT-1998; 98US-0105882P.
PR 27-OCT-1998; 98US-0106062P.
PR 28-OCT-1998; 98US-0106032P.
PR 28-OCT-1998; 98US-0106033P.
PR 28-OCT-1998; 98US-0106178P.
PR 29-OCT-1998; 98US-0106248P.
PR 29-OCT-1998; 98US-0106384P.
PR 29-OCT-1998; 98US-0108500P.
PR 30-OCT-1998; 98US-0106464P.
PR 03-NOV-1998; 98US-0106856P.
PR 03-NOV-1998; 98US-0106902P.
PR 03-NOV-1998; 98US-0106905P.
PR 03-NOV-1998; 98US-0106919P.
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PR 03-NOV-1998; 98US-0106934P.
PR 10-NOV-1998; 98US-0107783P.
PR 17-NOV-1998; 98US-0108775P.
PR 17-NOV-1998; 98US-0108779P.
PR 17-NOV-1998; 98US-0108787P.
PR 17-NOV-1998; 98US-0108788P.
PR 17-NOV-1998; 98US-0108801P.
PR 17-NOV-1998; 98US-0108802P.
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PR 17-NOV-1998; 98US-0108807P.
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PR 18-NOV-1998; 98US-0108849P.
PR 18-NOV-1998; 98US-0108850P.
PR 18-NOV-1998; 98US-0108851P.
PR 18-NOV-1998; 98US-0108852P.
PR 18-NOV-1998; 98US-0108858P.
PR 18-NOV-1998; 98US-0108904P.
PR 22-DEC-1998; 98US-0113296P.
PR 30-DEC-1998; 98US-0114223P.
PR 05-JAN-1999; 99WO-US000106.
PR 16-APR-1999; 99US-0129674P.
PR 23-JUN-1999; 99US-0141037P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
PR 01-SEP-1999; 99WO-US020111.
PR 15-SEP-1999; 99WO-US021194.
PR 29-OCT-1999; 99US-0162506P.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028551.
PR 16-DEC-1999; 99WO-US030095.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004342.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 15-MAR-2000; 2000WO-US006884.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.

000WO-US014941.
000WO-US015264.
000WO-US023522.
000WO-US023328.
000WO-US030952.
000WO-US030873.
000WO-US032678.
001WO-US006520.
001WO-US006666.
001WO-US017800.
001WO-US019692.
001WO-US021066.
001WO-US021735.
001US-00946374.

TECH INC.

stein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
ed A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
Wood WI;

93/55.
142.

i PRO polypeptides e.g. PRO1130, PRO1275, PRO1418, PRO1555,
modulate glucose or free fatty acid uptake by skeletal
and are useful for treating diabetes, hyper- or hypo-

100.0%; Score 609; DB 6; Length 117;
urity 100.0%; Pred.No.2e-63;
nservative 0; Mismatches 0; Indels 0; Gaps 0;

WAVFLASRLGGLLLTLEEHIAHFLGTGAATTMGNSICRDDSGTDSVDVTOQ 60
WAVFLASRLGGLLLTLEEHIAHFLGTGAATTMGNSICRDDSGTDSVDVTOQ 60

ISAVPTADTQRDPVRPRGRGPHPRKKQNVGLVLTFLAVIRTLVDK 117
ISAVPTADTQRDPVRPRGRGPHPRKKQNVGLVLTFLAVIRTLVDK 117

lard; protein; 117 AA.

First entry)

/transmembrane polypeptide PRO444.

d protein; transmembrane protein; PRO; VEGF inhibitor;
heial growth factor; endothelial cell proliferation;
roliferation; endothelial cell apoptosis;
ion; pancreatic beta cell differentiation;
oliferation; glucose uptake; free fatty acid; FFA uptake;

1.

002US-00066211.

97US-0056974P.
97US-0059115P.
97US-0059263P.
97US-0059588P.
97US-0062285P.
97US-0062816P.

24-OCT-1997; 97US-0063082P.
27-OCT-1997; 97US-0063329P.
29-OCT-1997; 97US-0063733P.
21-NOV-1997; 97US-006364P.
25-NOV-1997; 97US-0066840P.
16-DEC-1997; 97US-0069694P.
09-FEB-1998; 98US-0074086P.
09-FEB-1998; 98US-0074092P.
25-MAR-1998; 98US-0079294P.
08-APR-1998; 98US-0081049P.
14-JUL-1998; 98WO-US014552.
10-AUG-1998; 98US-0095988P.
18-AUG-1998; 98US-0097000P.
09-SEP-1998; 98US-0099601P.
10-SEP-1998; 98US-0099803P.
10-SEP-1998; 98US-0099811P.
10-SEP-1998; 98US-0099812P.
10-SEP-1998; 98WO-US018824.
14-SEP-1998; 98WO-US019093.
16-SEP-1998; 98WO-US019330.
17-SEP-1998; 98US-0100858P.
17-SEP-1998; 98WO-US019437.
24-SEP-1998; 98US-0101922P.
28-OCT-1998; 98US-0106032P.
20-NOV-1998; 98US-0109304P.
20-NOV-1998; 98WO-US024855.
25-NOV-1998; 98WO-US025190.
01-DEC-1998; 98WO-US025108.
08-MAR-1999; 99WO-US005028.
23-MAR-1999; 99US-0125778P.
02-JUN-1999; 99US-0139695P.
15-JUN-1999; 99US-0145070P.
26-JUL-1999; 99US-0145688P.
17-AUG-1999; 99US-0149396P.
01-SEP-1999; 99WO-US020111.
08-SEP-1999; 99WO-US020594.
15-SEP-1999; 99WO-US021090.
15-SEP-1999; 99WO-US021547.
30-NOV-1999; 99WO-US028313.
01-DEC-1999; 99WO-US028301.
02-DEC-1999; 99WO-US028565.
07-DEC-1999; 99US-0169495P.
20-DEC-1999; 99WO-US030999.
05-JAN-2000; 2000WO-US000219.
18-FEB-2000; 2000WO-US004341.
18-FEB-2000; 2000WO-US004342.
22-FEB-2000; 2000WO-US004414.
01-MAR-2000; 2000WO-US005601.
02-MAR-2000; 2000WO-US005841.
09-MAR-2000; 2000WO-US006471.
20-MAR-2000; 2000WO-US007377.
30-MAR-2000; 2000WO-US008439.
15-MAY-2000; 2000WO-US013358.
17-MAY-2000; 2000WO-US013705.
22-MAY-2000; 2000WO-US014042.
30-MAY-2000; 2000WO-US014941.
02-JUN-2000; 2000WO-US015264.
11-AUG-2000; 2000WO-US022031.
23-AUG-2000; 2000WO-US023522.
24-AUG-2000; 2000WO-US023328.
01-DEC-2000; 2000WO-US032678.
28-FEB-2001; 2001WO-US006520.
30-MAY-2001; 2001WO-US017443.
01-JUN-2001; 2001WO-US017800.
20-JUN-2001; 2001WO-US019692.
29-JUN-2001; 2001WO-US021066.
09-JUL-2001; 2001WO-US021735.
15-NOV-2001; 2001US-00002796.

(GETH) GENENTECH INC.

Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Eaton DL;

Tong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
 Gurney AL, Kijavini IJ, Mather JP, Napier MA, Pan J;
 Wy MA, Stewart TA, Tumas D, Watanabe CK, Williams PW;
 ing Z;
 1775/58.
 1180.
 d PRO polypeptides e.g. PRO365 and PRO187, useful for
 differentiation and/or proliferation of chondrocytes, and for
 ucose or free fatty acid uptake by skeletal muscle cells.
 13: 254pp; English.
 relates to an isolated secreted/transmembrane PRO
 The polypeptide and its nucleic acid is useful as an
 vascular endothelial growth factor stimulated proliferation
 d cells, as a stimulator of T-lymphocyte proliferation, as
 endothelial cell apoptosis, c-fos and differentiation of
 ta cell precursors into mature cell, for induction of
 tion and/or proliferation of chondrocytes and for modulating
 ee fatty acid (FFA) uptake by skeletal muscle cells. The
 and its nucleic acid is useful for generating transgenic or
 mals, for tissue typing and for chromosome identification.
 de is useful in a number of functional biological assays, as
 ght marker for protein electrophoresis, and as therapeutic
 nucleic acid is useful as a hybridisation probe, in
 d gene mapping, in the generation of antisense RNA and DNA,
 reparation PRO polypeptides. The nucleic acid is also useful
 ion probe for a cDNA library to isolate the full length PRO
 ate other cDNA and in gene therapy. The nucleic acid is also
 : construction of hybridisation probes for mapping the gene
 and for the genetic analysis of individuals with the
 ders. The present sequence represents the amino acid
 human secreted/transmembrane PRO polypeptide.
 AA;
 arity 100.0%; Score 609; DB 6; Length 117;
 onservative 0; Pred.No.2e-63;
 0; Mismatches 0; Indels 0; Gaps 0;
 GWAVFLASRLGQGLLLTLEBHIAHFLGTGGAATTMGNSICRDSGTDSDVDVTDQ 60
 GWAVFLASRLGQGLLLTLEBHIAHFLGTGGAATTMGNSICRDSGTDSDVDVTDQ 60
 NSAVPTADTRSQPRDVPVPPRGPHPRKKQNVGLVLDTLAVIRTLVDK 117
 NSAVPTADTRSQPRDVPVPPRGPHPRKKQNVGLVLDTLAVIRTLVDK 117
 dard; protein; 117 AA.
 (first entry)
 d/transmembrane protein PRO444.
 ed protein; transmembrane protein; PRO; vulnary; cardiant;
 anorectic; antiarthritic; angiogenesis; cancer;
 cal capillary; endothelial cell growth; wound healing;
 lymphocyte proliferation; immune response suppression;
 t hypertrophy; cardiac insufficiency disorder;
 rheial growth factor; inflammation; mononuclear cell;
 diabetes; obesity; or hyper-insulinaemia; hypo-insulinaemia;
 edifferentiation; bone disorder; cartilage disorder;
 ; arthritis.

PN US200304841-A1.
 XX 06-MAR-2003.
 XX
 XX 06-DEC-2001; 2001US-00006856.
 XX
 PR 01-SEP-1998; 98US-0098716P.
 PR 01-SEP-1998; 98US-0098723P.
 PR 01-SEP-1998; 98US-0098749P.
 PR 01-SEP-1998; 98US-0098750P.
 PR 02-SEP-1998; 98US-0098803P.
 PR 02-SEP-1998; 98US-0098821P.
 PR 02-SEP-1998; 98US-0098843P.
 PR 09-SEP-1998; 98US-0099536P.
 PR 09-SEP-1998; 98US-0099596P.
 PR 09-SEP-1998; 98US-0099598P.
 PR 09-SEP-1998; 98US-0099602P.
 PR 09-SEP-1998; 98US-0099642P.
 PR 10-SEP-1998; 98US-0099741P.
 PR 10-SEP-1998; 98US-0099754P.
 PR 10-SEP-1998; 98US-0099763P.
 PR 10-SEP-1998; 98US-0099792P.
 PR 10-SEP-1998; 98US-0099808P.
 PR 10-SEP-1998; 98US-0099812P.
 PR 10-SEP-1998; 98US-0099815P.
 PR 15-SEP-1998; 98US-0099816P.
 PR 15-SEP-1998; 98US-0100385P.
 PR 15-SEP-1998; 98US-0100388P.
 PR 15-SEP-1998; 98US-0100390P.
 PR 16-SEP-1998; 98US-0100584P.
 PR 16-SEP-1998; 98US-0100627P.
 PR 16-SEP-1998; 98US-0100661P.
 PR 16-SEP-1998; 98US-0100662P.
 PR 16-SEP-1998; 98US-0100664P.
 PR 17-SEP-1998; 98US-0100683P.
 PR 17-SEP-1998; 98US-0100684P.
 PR 17-SEP-1998; 98US-0100710P.
 PR 17-SEP-1998; 98US-0100711P.
 PR 17-SEP-1998; 98US-0100919P.
 PR 17-SEP-1998; 98US-0100930P.
 PR 18-SEP-1998; 98US-0100848P.
 PR 18-SEP-1998; 98US-0100849P.
 PR 18-SEP-1998; 98US-0101014P.
 PR 18-SEP-1998; 98US-0101068P.
 PR 18-SEP-1998; 98US-0101071P.
 PR 22-SEP-1998; 98US-0101279P.
 PR 23-SEP-1998; 98US-0101471P.
 PR 23-SEP-1998; 98US-0101472P.
 PR 23-SEP-1998; 98US-0101474P.
 PR 23-SEP-1998; 98US-0101475P.
 PR 23-SEP-1998; 98US-0101476P.
 PR 23-SEP-1998; 98US-0101477P.
 PR 23-SEP-1998; 98US-0101479P.
 PR 24-SEP-1998; 98US-0101738P.
 PR 24-SEP-1998; 98US-0101741P.
 PR 24-SEP-1998; 98US-0101743P.
 PR 24-SEP-1998; 98US-0101915P.
 PR 29-SEP-1998; 98US-0102207P.
 PR 29-SEP-1998; 98US-0102240P.
 PR 29-SEP-1998; 98US-0102307P.
 PR 29-SEP-1998; 98US-0102330P.
 PR 29-SEP-1998; 98US-0102331P.
 PR 30-SEP-1998; 98US-0102484P.
 PR 30-SEP-1998; 98US-0102487P.
 PR 30-SEP-1998; 98US-0102570P.
 PR 30-SEP-1998; 98US-0102571P.
 PR 01-OCT-1998; 98US-0102684P.
 PR 01-OCT-1998; 98US-0102687P.
 PR 02-OCT-1998; 98US-0102965P.
 PR 06-OCT-1998; 98US-0103258P.
 PR 06-OCT-1998; 98US-0103449P.
 PR 07-OCT-1998; 98US-0103314P.
 PR

PR	24-FEB-2000;	2000WO-US005004.	
PR	02-MAR-2000;	2000WO-US005841.	
PR	15-MAR-2000;	2000WO-US006884.	
PR	17-MAY-2000;	2000WO-US0113705.	
PR	22-MAY-2000;	2000WO-US0114042.	
PR	30-MAY-2000;	2000WO-US0114941.	
PR	02-JUN-2000;	2000WO-US0115264.	
PR	23-AUG-2000;	2000WO-US023522.	
PR	24-AUG-2000;	2000WO-US023328.	
PR	08-NOV-2000;	2000WO-US030952.	
PR	10-NOV-2000;	2000WO-US030873.	
PR	01-DEC-2000;	2000WO-US032678.	
PR	28-FEB-2001;	2001WO-US006520.	
PR	01-MAR-2001;	2001WO-US006666.	
PR	01-JUN-2001;	2001WO-US0117800.	
PR	20-JUN-2001;	2001WO-US0119692.	
PR	29-JUN-2001;	2001WO-US021066.	
PR	09-JUL-2001;	2001WO-US021735.	
PR	04-SEP-2001;	2001US-00946374.	
XX			
XX			
PA	(GETH) GENENTECH INC.		
PI	Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong		
PI	Gao XW, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hilla		
PI	Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Wata		
PI	Williams PM, Wood WI;		
XX			
XX	WPI; 2003-492259/46.		
DR	N-PSDB; ACH04344.		
DR			
XX			
PT	Novel secreted and transmembrane polypeptides and polynucleotides		
PT	encoding them useful for treating various cardiac insufficiency		
PT	disorders, bone and/or cartilage disorders such as sports injurie		
PT	arthritis.		
Query Match	100.0%;	Score 609;	DB 7; Length 117;
Best Local Similarity	100.0%;	Pred. NO. 2e-63;	Indels 0; G
Matches 117;	Conservative 0;	Mismatches 0;	
QY	1 MIVFGNAVFLASRLSGGLLLTLEEHIAHFLGTGGAATTMGNSCICRDDSGTDDSV		
Db	1 MIVFGNAVFLASRLSGGLLLTLEEHIAHFLGTGGAATTMGNSCICRDDSGTDDSV		
QY	61 QQAENSAPVTADTRSQPRDVPVPRPRGRGPHPRKKQNVGLVLDTLAVIRTLTV		
Db	61 QQAENSAPVTADTRSQPRDVPVPRPRGRGPHPRKKQNVGLVLDTLAVIRTLTV		
RESULT 10			
ABO33460			
ID	ABO33460 standard; protein; 117 AA.		
XX			
AC	ABO33460;		
XX			
DT	17-SEP-2003 (first entry)		
XX			
DE	Novel human secreted and transmembrane protein PRO444.		
XX			
KW	Human; secreted and transmembrane protein; PRO; gene therapy; vac		
KW	tissue typing; chromosome identification; vaccine.		
XX			
OS	Homo sapiens.		
XX			
PN	US2003073129-A1.		
XX			
PD	17-APR-2003.		
XX			
XX	04-SEP-2001; 2001US-00946374.		
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PR	01-SEP-1998; 98US-00987116P.		
PR	01-SEP-1998; 98US-0098723P.		
PR	01-SEP-1998; 98US-0098749P.		
PR	01-SEP-1998; 98US-0098750P.		

98US-0098803P.
98US-0098821P.
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98US-0099741P.
98US-0099754P.
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98US-0104257P.

20-OCT-1998;
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02-DEC-1999;
16-DEC-1999;
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22-MAY-2000;
30-MAY-2000;
02-JUN-2000;
23-AUG-2000;
98US-0104987P.
98US-0105000P.
98US-0105002P.
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98US-0108858P.
98US-0108904P.
98US-00218517.
98US-0113296P.
98US-0114223P.
99WO-US000106.
99US-00284291.
99US-0129674P.
99US-0141037P.
99US-0144758P.
99US-0145698P.
99WO-US020111.
99WO-US021194.
99US-00403297.
99WO-US028313.
99WO-US028551.
99WO-US030095.
2000WO-US000219.
2000WO-US000376.
2000WO-US003565.
2000WO-US004342.
2000WO-US005004.
2000WO-US005841.
2000WO-US006884.
2000WO-US013705.
2000WO-US014042.
2000WO-US014941.
2000WO-US015264.
2000WO-US023522.

000WO-US023328.
000WO-US030952.
000WO-US030873.
000WO-US032678.
001WO-US008520.
001WO-US008666.
001US-00872035.
001WO-US017800.
001US-00882636.
001WO-US019692.
001WO-US021066.
001WO-US021735.
ECH INC.
stein D, Desnoyers L, Eaton DL, Ferrava N, Fong S;
d A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KU;
NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
Wood WI;
92/55.
88.
PRO polypeptides e.g. PRO1491 and PRO1571, useful in the
a medicament for treating a condition responsive to PRO
nd as therapeutic agents e.g. vaccines.
4; 561pp; English.
describes an isolated PRO (secreted and transmembrane)
, having at least 80% sequence identity to a sequence
100.0%; Score 609; DB 7; Length 117;
urity 100.0%; Pred. No. 2e-63;
nservative 0; Mismatches 0; Indels 0; Gaps 0;
WAVFLASRLGQGLLLTLEEHIAHFLGTGGAATTGNSICRDSGTDSDVDTQ 60
WAVFLASRLGQGLLLTLEEHIAHFLGTGGAATTGNSICRDSGTDSDVDTQ 60
ISAVPTADTESQPRDVPRRRGPGPHEPRKKQNDGLVLDLAVIRTLVDK 117
ISAVPTADTESQPRDVPRRRGPGPHEPRKKQNDGLVLDLAVIRTLVDK 117
lard; protein; 117 AA.
(first entry)
l/transmembrane protein PRO444.
creted and transmembrane protein; gene therapy;
Gastrointestinal ulceration; skin disease; asthma;
inocyte differentiation; psoriasis; epithelial cancer;
carcinoma; Alzheimer's disease; Parkinson's disease;
lateral sclerosis; inflammatory disease; organ failure;
thritis; multiple sclerosis; atherosclerosis; infertility;
/; birth defect; premature aging; AIDS; cancer;
lication; wound repair.
11.
2002US-00066193.
97US-0056974P.

17-SEP-1997; 97US-0059115P.
18-SEP-1997; 97US-0059263P.
19-SEP-1997; 97US-0059588P.
17-OCT-1997; 97US-0062285P.
24-OCT-1997; 97US-0062816P.
24-OCT-1997; 97US-0063082P.
27-OCT-1997; 97US-0063329P.
29-OCT-1997; 97US-0063733P.
21-NOV-1997; 97US-0066364P.
25-NOV-1997; 97US-0066840P.
16-DEC-1997; 97US-006694P.
09-FEB-1998; 98US-0074086P.
09-FEB-1998; 98US-0074092P.
25-MAR-1998; 98US-0079294P.
08-APR-1998; 98US-0081049P.
10-AUG-1998; 98US-0095998P.
18-AUG-1998; 98US-0097000P.
09-SEP-1998; 98US-0099601P.
10-SEP-1998; 98US-0099803P.
10-SEP-1998; 98US-0099811P.
14-SEP-1998; 98US-0099812P.
14-SEP-1998; 98WO-US019093.
16-SEP-1998; 98WO-US019330.
17-SEP-1998; 98US-0100858P.
17-SEP-1998; 98WO-US019437.
24-SEP-1998; 98US-0101922P.
28-OCT-1998; 98US-0106032P.
20-NOV-1998; 98US-0109304P.
20-NOV-1998; 98WO-US024855.
25-NOV-1998; 98WO-US025190.
01-DEC-1998; 98WO-US025108.
08-MAR-1999; 99WO-US005028.
23-MAR-1999; 99US-0125778P.
02-JUN-1999; 99WO-US012252.
15-JUN-1999; 99US-0139695P.
20-JUL-1999; 99US-0145070P.
26-JUL-1999; 99US-0145698P.
17-AUG-1999; 99US-0149396P.
01-SEP-1999; 99WO-US020111.
08-SEP-1999; 99WO-US020594.
15-SEP-1999; 99WO-US021090.
15-SEP-1999; 99WO-US021547.
30-NOV-1999; 99WO-US028313.
01-DEC-1999; 99WO-US028301.
02-DEC-1999; 99WO-US028565.
07-DEC-1999; 99US-0169495P.
20-DEC-1999; 99WO-US030999.
05-JAN-2000; 2000WO-US000219.
18-FEB-2000; 2000WO-US004341.
18-FEB-2000; 2000WO-US004342.
22-FEB-2000; 2000WO-US004414.
01-MAR-2000; 2000WO-US005601.
02-MAR-2000; 2000WO-US005841.
03-MAR-2000; 2000WO-US006471.
20-MAR-2000; 2000WO-US007377.
30-MAR-2000; 2000WO-US008439.
15-MAY-2000; 2000WO-US013358.
17-MAY-2000; 2000WO-US013705.
22-MAY-2000; 2000WO-US014042.
30-MAY-2000; 2000WO-US014941.
02-JUN-2000; 2000WO-US015264.
11-AUG-2000; 2000WO-US022031.
23-AUG-2000; 2000WO-US023522.
24-AUG-2000; 2000WO-US023328.
01-DEC-2000; 2000WO-US032678.
28-FEB-2001; 2001WO-US006520.
30-MAY-2001; 2001WO-US017443.
01-JUN-2001; 2001WO-US017800.
20-JUN-2001; 2001WO-US019692.
29-JUN-2001; 2001WO-US021066.
09-JUL-2001; 2001WO-US021735.
15-NOV-2001; 2001US-00002796.
XX

TECH INC.

Baker KP, Botstein DA, Desnoyers L, Eaton DL;
 'ong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
 Gurney AL, Kljavin IJ, Mather JP, Napier MA, Pan J;
 Y MA, Stewart TA, Tumas D, Watanabe CK, Williams EM;
 ng Z;

261/46.
 202.

peptides and nucleic acid molecules, useful in diagnosing or
 amatory diseases, organ failure, atherosclerosis, cardiac
 tility, cancer, AIDS, Alzheimer's disease or Parkinson's

[4; 154pp; English.

relates to an isolated native sequence PRO polypeptide
 (transmembrane protein) having 80% sequence similarity to
 eins sequences (or PRO lacking its signal peptide, a PRO
 domain (with or without a signal peptide) encoded by a
 : 80% identical to one of 37 cDNA sequences, shown in the
 : Also included are vectors comprising the PRO nucleic
 : cells comprising the vectors (used to produce the PRO
 : chimaeric molecule comprising the PRO polypeptide fused to a
 : amino acid sequence, an anti-PRO antibody, linking a
 : scule to a cell expressing the PRO polypeptides and
 : least one biological activity of a cell expressing the
 : The PRO polypeptides and nucleic acids are useful in
 : treating enterocolitis, gastrointestinal ulceration, skin
 : ciated with abnormal keratinocyte differentiation, e.g.
 : epithelial cancers such as squamous cell carcinoma,
 : disease, Parkinson's disease, amyotrophic lateral sclerosis,
 : diseases, e.g. rheumatoid arthritis, asthma or multiple
 : gan failure, atherosclerosis, cardiac injury, infertility,
 : premature aging, AIDS, cancer, diabetic complications, or
 : general. The polypeptides are also useful for wound repair
 : d therapies concerned with re-growth of tissue. The
 : nquences may be used as hybridisation probes in chromosome
 : ing, or in generating antisense RNA and DNA. PRO nucleic
 : o useful in preparing PRO polypeptides, in assays to
 : r proteins or molecules involved in binding reaction, to
 : agenic animals or knockout animals, which in turn are useful
 : pment and screening of therapeutically useful reagents, for
 : ntification, and tissue typing. The PRO polypeptides and
 : molecules are also useful in gene therapy, and as molecular
 : s for protein electrophoresis purposes. The anti-PRO
 : y be used in diagnostic assays for PRO, or for the affinity
 : of PRO from recombinant cell culture or natural sources. The
 : nce represents a PRO protein of the invention

AA;

100.0%; Score 609; DB 7; Length 117;
 arity 100.0%; Pred. No. 2e-63;
 onservative 0; Mismatches 0; Indels 0; Gaps 0;

'GWAFLASRLGQGLLLLEEHIAHFLGTGGAATMGNSICRDBSDGSDSDVDTQ 60

'GWAFLASRLGQGLLLLEEHIAHFLGTGGAATMGNSICRDBSDGSDSDVDTQ 60

INSAVTADTRSQPRPVRPPRGPHPRKQKQVNDGLVLDLAVIRTLVDK 117

INSAVTADTRSQPRPVRPPRGPHPRKQKQVNDGLVLDLAVIRTLVDK 117

idard; protein; 117 AA.

DT 18-DEC-2003 (first entry)
 XX Human PRO polypeptide #2.
 DE Human; PRO; protein electrophoresis; chromosome mapping; gene map;
 XX genetic disorder.
 KW Homo sapiens.
 XX OS
 XX US2003064925-A1.
 PN 03-APR-2003.
 PD
 XX 10-DEC-2001; 2001US-00013907.
 PF 01-SEP-1998; 98US-0098716P.
 PR 01-SEP-1998; 98US-0098723P.
 PR 01-SEP-1998; 98US-0098749P.
 PR 01-SEP-1998; 98US-0098750P.
 PR 02-SEP-1998; 98US-0098803P.
 PR 02-SEP-1998; 98US-0098821P.
 PR 02-SEP-1998; 98US-0098843P.
 PR 09-SEP-1998; 98US-0099536P.
 PR 09-SEP-1998; 98US-0099596P.
 PR 09-SEP-1998; 98US-0099598P.
 PR 09-SEP-1998; 98US-0099602P.
 PR 09-SEP-1998; 98US-0099642P.
 PR 10-SEP-1998; 98US-0099741P.
 PR 10-SEP-1998; 98US-0099754P.
 PR 10-SEP-1998; 98US-0099763P.
 PR 10-SEP-1998; 98US-0099792P.
 PR 10-SEP-1998; 98US-0099808P.
 PR 10-SEP-1998; 98US-0099812P.
 PR 10-SEP-1998; 98US-0099815P.
 PR 15-SEP-1998; 98US-0100385P.
 PR 15-SEP-1998; 98US-0100388P.
 PR 15-SEP-1998; 98US-0100390P.
 PR 16-SEP-1998; 98US-0100584P.
 PR 16-SEP-1998; 98US-0100627P.
 PR 16-SEP-1998; 98US-0100661P.
 PR 16-SEP-1998; 98US-0100662P.
 PR 16-SEP-1998; 98US-0100664P.
 PR 17-SEP-1998; 98US-0100683P.
 PR 17-SEP-1998; 98US-0100684P.
 PR 17-SEP-1998; 98US-0100710P.
 PR 17-SEP-1998; 98US-0100711P.
 PR 17-SEP-1998; 98US-0100919P.
 PR 17-SEP-1998; 98US-0100930P.
 PR 18-SEP-1998; 98US-0100848P.
 PR 18-SEP-1998; 98US-0100849P.
 PR 18-SEP-1998; 98US-0101014P.
 PR 18-SEP-1998; 98US-0101068P.
 PR 18-SEP-1998; 98US-0101071P.
 PR 22-SEP-1998; 98US-0101279P.
 PR 23-SEP-1998; 98US-0101471P.
 PR 23-SEP-1998; 98US-0101472P.
 PR 23-SEP-1998; 98US-0101474P.
 PR 23-SEP-1998; 98US-0101475P.
 PR 23-SEP-1998; 98US-0101476P.
 PR 23-SEP-1998; 98US-0101477P.
 PR 23-SEP-1998; 98US-0101479P.
 PR 24-SEP-1998; 98US-0101738P.
 PR 24-SEP-1998; 98US-0101741P.
 PR 24-SEP-1998; 98US-0101743P.
 PR 24-SEP-1998; 98US-0101915P.
 PR 24-SEP-1998; 98US-0101916P.
 PR 29-SEP-1998; 98US-0102207P.
 PR 29-SEP-1998; 98US-0102240P.
 PR 29-SEP-1998; 98US-0102307P.
 PR 29-SEP-1998; 98US-0102330P.
 PR 29-SEP-1998; 98US-0102331P.
 PR 30-SEP-1998; 98US-0102484P.

98US-0102487P.
 98US-0102570P.
 98US-0102571P.
 98US-0102684P.
 98US-0102687P.
 98US-0102965P.
 98US-0103258P.
 98US-0103449P.
 98US-0103314P.
 98US-0103315P.
 98US-0103328P.
 98US-0103335P.
 98US-0103396P.
 98US-0103401P.
 98US-0103633P.
 98US-0103678P.
 98US-0103679P.
 98US-0103711P.
 98US-0104257P.
 98US-0104987P.
 98US-0105000P.
 98US-0105002P.
 98US-0105104P.
 98US-0105169P.
 98US-0105266P.
 98US-0105693P.
 98US-0105694P.
 98US-0105807P.
 98US-0105881P.
 98US-0105882P.
 98US-0106062P.
 98US-0106023P.
 98US-0106029P.
 98US-0106030P.
 98US-0106032P.
 98US-0106033P.
 98US-0106178P.
 98US-0106248P.
 98US-0106384P.
 98US-0108500P.
 98US-0106464P.
 98US-0106856P.
 98US-0106902P.
 98US-0106905P.
 98US-0106919P.
 98US-0106932P.
 98US-0106934P.
 98US-0107783P.
 98US-0108775P.
 98US-0108779P.
 98US-0108787P.
 98US-0108788P.
 98US-0108801P.
 98US-0108802P.
 98US-0108806P.
 98US-0108807P.
 98US-0108867P.
 98US-0108925P.
 98US-0108848P.
 98US-0108849P.
 98US-0108850P.
 98US-0108851P.
 98US-0108852P.
 98US-0108858P.
 98US-0108904P.
 98US-0113296P.
 98US-0114223P.
 99WO-US000106.
 99US-0129674P.
 99US-0141037P.
 99US-0144758P.
 99US-0145698P.
 99WO-US020111.

PR 15-SEP-1999; 99WO-US0211194.
 PR 29-OCT-1999; 99US-0162506P.
 PR 30-NOV-1999; 99WO-US028313.
 PR 02-DEC-1999; 99WO-US028551.
 PR 16-DEC-1999; 99WO-US030095.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 06-JAN-2000; 2000WO-US003376.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 24-FEB-2000; 2000WO-US005004.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 15-MAR-2000; 2000WO-US006884.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 08-NOV-2000; 2000WO-US030952.
 PR 10-NOV-2000; 2000WO-US030873.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 01-MAR-2001; 2001WO-US006666.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 04-SEP-2001; 2001US-00946374.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong
 PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hilla
 PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Wata
 PI Williams PM, Wood WI;
 XX WPI; 2003-555602/52.
 DR N-PSDB; ADC17874.
 XX
 PT Novel isolated PRO polypeptides e.g. PRO1491 and PRO1571, useful
 PT preparation of a medicament for treating a condition responsive to
 PT polypeptide, and as therapeutic agents e.g. vaccines.
 XX
 PS Claim 12; SEQ ID NO 6; 555pp; English.
 XX
 CC The invention relates to human PRO polypeptides and the polynucle
 CC encoding them. The sequences are useful in the preparation of a
 CC medicament for treating a condition responsive to a PRO polypepti
 CC polypeptides are useful in a number of functional biological assa
 CC molecular weight markers for protein electrophoresis and as thera
 CC
 Query Match 100.0%; Score 609; DB 7; Length 117;
 Best Local Similarity 100.0%; Pred. No. 2e-63;
 Matches 117; Conservative 0; Mismatches 0; Indels 0; G
 Qy 1 MIVFGWAVFLASRLSGQLLLTLEEHIAHFLGTGGAATTMGNSCICRDSSTDSV
 Db 1 MIVFGWAVFLASRLSGQLLLTLEEHIAHFLGTGGAATTMGNSCICRDSSTDSV
 Qy 61 QQAENSAPTADTRSPRPVPRGRGPHPRKKQNVGLVLTAVIRTLVD
 Db 61 QQAENSAPTADTRSPRPVPRGRGPHPRKKQNVGLVLTAVIRTLVD
 RESULT 13
 ADD10295
 ID ADD10295 standard; protein; 117 AA.
 XX
 AC ADD10295;
 XX
 DT 01-JAN-2004 (first entry)
 XX
 DE Human secreted/transmembrane PRO polypeptide #3.

ted protein; transmembrane protein; cardiovascular disorder;
disorder; angiogenic disorder; myocardial infarction;
ctrophy; trauma; cancer; age-related macular degeneration;
endothelial cell apoptosis; smooth muscle cell growth;
cell tube formation.

-A1.

2002US-00223084.

2000US-0232887P.

2001WO-US019692.

2001WO-US021735.

2002US-00081056.

NTech INC.

Ferrara N, Gerber H, Gerritsen ME, Goddard A;

Gurney AL, Hillan KJ, Marsters SA, Pan J, Stephan JF;

Williams PM, Wood WI, Ye W;

0831/76.

0294.

nucleic acid encoding a secreted and transmembrane

for treating a cardiovascular, endothelial, or angiogenic

a mammal, such as cancer or age-related macular degeneration.

ID NO 6; 493pp; English.

relates to an isolated nucleic acid encoding a secreted and
polypeptide (PRO). The nucleic acid, a polypeptide encoded
c acid, or an agonist or antagonist, is used to treat a
ir, endothelial, or angiogenic disorder in a mammal,
human. The human may have suffered a myocardial infarction
ic hypertrophy, trauma, a cancer, or age-related macular

The cardiac hypertrophy is characterized by the presence of
level of PGF-2 alpha. A PRO polypeptide, given in the
i, or an agonist is used to inhibit or stimulate endothelial

n a mammal. PRO21 or an agonist is used to induce cardiac
PRO1376 or PRO1449 is used to stimulate angiogenesis.

agonist is used to induce endothelial cell apoptosis. A PRO
given in the specification, or an agonist is used to
inhibit smooth muscle cell growth, or to induce endothelial

mation. The present sequence represents the amino acid

PRO polypeptide of the invention.

AA;

100.0%; Score 609; DB 7; Length 117;

arity 100.0%; Pred. No. 2e-63; Mismatches 0; Indels 0; Gaps 0;

onservative 0; Mismatches 0; Indels 0; Gaps 0;

WAVFLASRLGQGLLLTLEEHIAHFLGTGGATTMGNSICRDRDSDGTDGQ 60

WAVFLASRLGQGLLLTLEEHIAHFLGTGGATTMGNSICRDRDSDGTDGQ 60

WAVFLASRLGQGLLLTLEEHIAHFLGTGGATTMGNSICRDRDSDGTDGQ 60

WAVFLASRLGQGLLLTLEEHIAHFLGTGGATTMGNSICRDRDSDGTDGQ 60

WAVFLASRLGQGLLLTLEEHIAHFLGTGGATTMGNSICRDRDSDGTDGQ 60

WAVFLASRLGQGLLLTLEEHIAHFLGTGGATTMGNSICRDRDSDGTDGQ 60

WAVFLASRLGQGLLLTLEEHIAHFLGTGGATTMGNSICRDRDSDGTDGQ 60

WAVFLASRLGQGLLLTLEEHIAHFLGTGGATTMGNSICRDRDSDGTDGQ 60

WAVFLASRLGQGLLLTLEEHIAHFLGTGGATTMGNSICRDRDSDGTDGQ 60

WAVFLASRLGQGLLLTLEEHIAHFLGTGGATTMGNSICRDRDSDGTDGQ 60

WAVFLASRLGQGLLLTLEEHIAHFLGTGGATTMGNSICRDRDSDGTDGQ 60

WAVFLASRLGQGLLLTLEEHIAHFLGTGGATTMGNSICRDRDSDGTDGQ 60

WAVFLASRLGQGLLLTLEEHIAHFLGTGGATTMGNSICRDRDSDGTDGQ 60

WAVFLASRLGQGLLLTLEEHIAHFLGTGGATTMGNSICRDRDSDGTDGQ 60

WAVFLASRLGQGLLLTLEEHIAHFLGTGGATTMGNSICRDRDSDGTDGQ 60

WAVFLASRLGQGLLLTLEEHIAHFLGTGGATTMGNSICRDRDSDGTDGQ 60

WAVFLASRLGQGLLLTLEEHIAHFLGTGGATTMGNSICRDRDSDGTDGQ 60

WAVFLASRLGQGLLLTLEEHIAHFLGTGGATTMGNSICRDRDSDGTDGQ 60

WAVFLASRLGQGLLLTLEEHIAHFLGTGGATTMGNSICRDRDSDGTDGQ 60

WAVFLASRLGQGLLLTLEEHIAHFLGTGGATTMGNSICRDRDSDGTDGQ 60

WAVFLASRLGQGLLLTLEEHIAHFLGTGGATTMGNSICRDRDSDGTDGQ 60

01-JAN-2004 (first entry)

Human secreted/transmembrane PRO polypeptide #3.

human; secreted protein; transmembrane protein; cardiovascular d
endothelial disorder; angiogenic disorder; myocardial infarction
cardiac hypertrophy; trauma; cancer; age-related macular degener
angiogenesis; endothelial cell apoptosis; smooth muscle cell gro
endothelial cell tube formation.

Homo sapiens.

US2003105013-A1.

05-JUN-2003.

16-AUG-2002; 2002US-00223090.

20-JUN-2001; 2001WO-US019692.

09-JUL-2001; 2001WO-US021735.

20-FEB-2002; 2002US-00081056.

20-FEB-2002; 2002US-00081056.

20-FEB-2002; 2002US-00081056.

20-FEB-2002; 2002US-00081056.

20-FEB-2002; 2002US-00081056.

20-FEB-2002; 2002US-00081056.

20-FEB-2002; 2002US-00081056.

20-FEB-2002; 2002US-00081056.

20-FEB-2002; 2002US-00081056.

20-FEB-2002; 2002US-00081056.

20-FEB-2002; 2002US-00081056.

20-FEB-2002; 2002US-00081056.

20-FEB-2002; 2002US-00081056.

20-FEB-2002; 2002US-00081056.

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20-FEB-2002; 2002US-00081056.

20-FEB-2002; 2002US-00081056.

20-FEB-2002; 2002US-00081056.

20-FEB-2002; 2002US-00081056.

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20-FEB-2002; 2002US-00081056.

20-FEB-2002; 2002US-00081056.

20-FEB-2002; 2002US-00081056.

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20-FEB-2002; 2002US-00081056.

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20-FEB-2002; 2002US-00081056.

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20-FEB-2002; 2002US-00081056.

20-FEB-2002; 2002US-00081056.

20-FEB-2002; 2002US-00081056.

20-FEB-2002; 2002US-00081056.

20-FEB-2002; 2002US-00081056.

20-FEB-2002; 2002US-00081056.

20-FEB-2002; 2002US-00081056.

DT

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01-JAN-2004 (first entry)

Human secreted/transmembrane PRO polypeptide #3.

human; secreted protein; transmembrane protein; cardiovascular d
endothelial disorder; angiogenic disorder; myocardial infarction
cardiac hypertrophy; trauma; cancer; age-related macular degener
angiogenesis; endothelial cell apoptosis; smooth muscle cell gro
endothelial cell tube formation.

Homo sapiens.

US2003105013-A1.

05-JUN-2003.

16-AUG-2002; 2002US-00223090.

20-JUN-2001; 2001WO-US019692.

09-JUL-2001; 2001WO-US021735.

20-FEB-2002; 2002US-00081056.

20-FEB-2002; 2002US-00081056.

20-FEB-2002; 2002US-00081056.

20-FEB-2002; 2002US-00081056.

20-FEB-2002; 2002US-00081056.

20-FEB-2002; 2002US-00081056.

20-FEB-2002; 2002US-00081056.

20-FEB-2002; 2002US-00081056.

20-FEB-2002; 2002US-00081056.

20-FEB-2002; 2002US-00081056.

20-FEB-2002; 2002US-00081056.

20-FEB-2002; 2002US-00081056.

20-FEB-2002; 2002US-00081056.

20-FEB-2002; 2002US-00081056.

20-FEB-2002; 2002US-00081056.

20-FEB-2002; 2002US-00081056.

20-FEB-2002; 2002US-00081056.

20-FEB-2002; 2002US-00081056.

20-FEB-2002; 2002US-00081056.

20-FEB-2002; 2002US-00081056.

20-FEB-2002; 2002US-00081056.

20-FEB-2002; 2002US-00081056.

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 104

98US-0114223P.
99WO-US000106.
99US-0129674P.
99US-0141037P.
99US-0144758P.
99US-0145698P.
99WO-US020111.
99WO-US021194.
99US-0162506P.
99WO-US028313.
99WO-US028551.
99WO-US030095.
2000WO-US000219.
2000WO-US000376.
2000WO-US003565.
2000WO-US004342.
2000WO-US005004.
2000WO-US005841.
2000WO-US006884.
2000WO-US013705.
2000WO-US014042.
2000WO-US014941.
2000WO-US015264.
2000WO-US023522.
2000WO-US023328.
2000WO-US030952.
2000WO-US030873.
2000WO-US032678.
2001WO-US006520.
2001WO-US006666.
2001WO-US017800.
2001WO-US019692.
2001WO-US021066.
2001WO-US021735.
2001US-00946374.

TECH INC.

tstein D, Deanyers L, Eaton DL, Ferrara N, Fong S;
rd A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
Wood WI;

502/81.
520.

i PRO polypeptides e.g., PRO1130, PRO1275, PRO1418, PRO1555,
t glucose or free fatty acid (FFA) uptake by skeletal muscle
useful for treating diabetes or hyper- or hypo-insulinemia.

ID NO 6; 553pp; English.

relates to an isolated PRO polypeptide (secreted or

100.0%; Score 609; DB 7; Length 117;
arity 100.0%; Pred. No. 2e-63;
nservative 0; Mismatches 0; Indels 0; Gaps 0;

3WAVFLASRLGQGLLTLEEHIAHFLGTGGAATTMGNSICRDDSGTDDSDVTQQ 60

3WAVFLASRLGQGLLTLEEHIAHFLGTGGAATTMGNSICRDDSGTDDSDVTQQ 60

NSAVPTADTRSQPRDPVPPRRGPGHPHPRKKQNVGLVLDTLAVIRTLVDK 117

NSAVPTADTRSQPRDPVPPRRGPGHPHPRKKQNVGLVLDTLAVIRTLVDK 117

April 2, 2004, 10:24:42

GenCore version 5.1.6
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in search, using sw model

File 2, 2004, 10:12:49 ; Search time 17 Seconds
(without alignments)
358.365 Million cell updates/sec

10-066-273-9

11VFGWAVFLASRLQGLL.....QNVDELVLTLAVIRTLVDK 117

SUM62

top 10.0 , Gapext 0.5

681 seqs, 52070155 residues

s satisfying chosen parameters: 141681

idh: 0

idh: 2000000000

Minimum Match 0%

Maximum Match 100%

string first 45 summaries

MassProt_42.*

the number of results predicted by chance to have a
than or equal to the score of the result being printed,
ed by analysis of the total score distribution.

SUMMARIES

ID	Length	DB	ID	Description
1.0	612	1	THIC_STRCO	Q9x9u0 streptomyc
1.9	188	1	SSB_ALCEU	P59927 alcaligenes
1.8	1483	1	BALB_HUMAN	Q9u1g0 homo sapien
1.3	286	1	MSA2_PLAF1	P50496 plasmodium
1.1	2505	1	CCAA_HUMAN	O00555 homo sapien
1.0	281	1	MSA2_PLAFH	Q99319 plasmodium
1.0	353	1	TGNI_MOUSE	P62313 mus musculus
1.0	1466	1	CA13_HUMAN	P02461 homo sapien
1.9	262	1	MSA2_PLAF7	Q99317 plasmodium
1.9	272	1	MSA2_PLAF6	P50498 plasmodium
1.9	274	1	MSA2_PLAF7	P50497 plasmodium
1.9	287	1	MSA2_PLAF6	P19260 plasmodium
1.9	300	1	MSA2_PLAF1	Q03644 plasmodium
1.9	300	1	MSA2_PLAF2	Q03645 plasmodium
1.9	302	1	MSA2_PLAF9	Q03994 plasmodium
1.9	347	1	MSA2_PLAF2	Q03646 plasmodium
1.9	458	1	YNE1_CAEEL	P30640 caenorhabdi
1.8	1787	1	CHD3_CAEEL	Q22516 caenorhabdi
1.7	1479	1	BALB_MOUSE	Q9z277 mus musculus
1.6	3726	1	TRX_DROME	P20659 drosophila
1.5	445	1	NRH3_MOUSE	Q9z0y9 mus musculus
1.3	1944	1	CHD3_HUMAN	Q12873 homo sapien
1.2	424	1	COT1_BOVIN	Q9trr8 bos taurus
1.2	445	1	NRH3_RAT	Q62685 rattus norv
1.2	504	1	FTSV_SYNY3	P73930 synechocyst
1.2	702	1	EXO1_YEAST	P39875 saccharomyc
1.1	399	1	SIR3_HUMAN	Q9ntg7 homo sapien
1.1	727	1	CTCF_HUMAN	P49711 homo sapien
1.1	1298	1	ICP4_HSV11	P08392 herpes simp
1.0	393	1	CIM4_HUMAN	Q9nyg8 homo sapien
1.0	1202	1	NOS3_HUMAN	P29474 homo sapien
1.0	3828	1	TRX_DROVI	Q24742 drosophila
1.9	217	1	YKR4_EBV	P30117 epstein-bar

34	66.5	10.9	268	1	EP34_HCMVA	P16768 huma
35	66.5	10.9	276	1	MSA2_PLAF8	Q99320 plas
36	66.5	10.9	343	1	GLN2_STRVR	P19432 stre
37	66.5	10.9	423	1	COT1_HUMAN	P10589 homo
38	66.5	10.9	684	1	EP84_HCMVA	P17151 huma
39	66	10.8	228	1	EFAS_HUMAN	P52803 homo
40	66	10.8	228	1	EFAS_MOUSE	O08543 mus
41	66	10.8	324	1	HE31_STRAW	Q82e76 stre
42	66	10.8	736	1	DVL2_XENLA	P51142 xeno
43	66	10.8	1021	1	MAPA_MOUSE	Q9qy76 mus
44	66	10.8	1380	1	CYAP_LEIDO	Q27675 leis
45	66	10.8	2716	1	OSA_DROME	Q9in94 dros

ALIGNMENTS

RESULT 1
THIC_STRCO STANDARD; PRT; 612 AA.
ID AC Q9X9U0;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Thiamine biosynthesis protein thic.
GN THIC OR SC03928 OR SCQ11.11.
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RX MEDLINE=21996410; PubMed=12000953;
RA Bentley S.D.; Chater K.F.; Cerdano-Tarraga A.-M.; Challis G.L.;
Thomson N.R.; James K.D.; Harris D.E.; Quail M.A.; Kleser H.;
Harper D.; Bateman A.; Brown S.; Chandra G.; Chen C.W.; Collins M.
Cronin A.; Fraser A.; Goble A.; Hidalgo J.; Hornsby T.; Howarth S.
Huang C.-H.; Kleser T.; Larke L.; Murphy L.; Oliver K.; O'Neill S.
Rabinovitch E.; Rajandream M.A.; Rutherford K.; Rutter S.;
Seeger K.; Saunders D.; Sharp S.; Squares R.; Squares S.; Taylor I.
Warren T.; Wietzorrek A.; Woodward J.; Barrell B.G.; Parkhill J.;
Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
coelicolor A3(2).";
RL Nature 417:141-147(2002).
CC -!- FUNCTION: Required for the synthesis of the hydromethylpyrimi-
(HMP) moiety of thiamine (4-amino-2-methyl-5-
hydroxymethylpyrimidine) (By similarity).
CC -!- PATHWAY: Thiamine biosynthesis.
CC -!- SIMILARITY: Belongs to the thic family.
CC This SWISS-PROT entry is copyright. It is produced through a coll-
between the Swiss Institute of Bioinformatics and the EMBL out-
the European Bioinformatics Institute. There are no restriction:
use by non-profit institutions as long as its content is in
modified and this statement is not removed. Usage by and for c-
entities requires a license agreement (See <http://www.isb-sib.ch/>;
or send an email to license@isb-sib.ch).
CC
CC EMBL; AL939118; CAB46966.1; -.
DR PIR; T37181; T37181.
DR HAMAP; MF 00089; -; 1.
DR InterPro; IPR002817; Thic.
DR Pfam; PF01964; Thic; 1.
DR ProDom; PD007048; Thic; 1.
DR TIGRFAMs; TIGR00190; thic; 1.
KW Thiamine biosynthesis; Complete proteome.
SQ SEQUENCE 612 AA; 67371 MW; 290BF2454200CF68 CRC64;

Query Match 13.0%; Score 79; DB 1; Length 612;
Best Local Similarity 31.2%; Pred. No. 2.4;
Matches 30; Conservative 7; Mismatches 37; Indels 22; G;

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NSCICRDSG--TDSVDYTOOQA-----NSAVPTADTRSPQRPDPVRP----- 83
GN ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OS QSVTLXTDTPYTDLPDVTDRGLAPLRNWLIIARGDTEYAGRPVRPDDGKHT 119
OC ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OC RGRG-----PHEPRRKQNVGDLVLTAVIR 112
ON ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
RN GGLRNLDVAFPRGRPRGRDGNVATQLAYAR 155

STANDARD; PRT; 188 AA.
07; (Rel. 43, Created)
08; (Rel. 43, Last sequence update)
09; (Rel. 43, Last annotation update)
10; d binding protein (SSB) (Helix-destabilizing protein).
11;
12; 5.
13; eutrophus (Ralstonia eutropha).
14; plasmid pHG1.
15; cteobacteria; Betaproteobacteria; Burkholderiales;
16; ceae; Ralstonia.
17; 10;
18; 4 N.A.
19; DSM 428 / ATCC 17699;
20; Henne A., Cramm R., Eitinger T., Friedrich B.,
21; .;
22; clectide sequence of pHG1: a Ralstonia eutropha H16
23; encoding key enzymes of H2-based lithoautotrophy and
24; .;
25; . 332:369-383(2003).
26; .; This protein is essential for replication of the
27; me. It is also involved in DNA recombination and repair
28; larity).
29; TY: Contains 1 SSB domain.
30; -----
31; ROT entry is copyright. It is produced through a collaboration
32; Swiss Institute of Bioinformatics and the EMBL outstation -
33; Bioinformatics Institute. There are no restrictions on its
34; -profit institutions as long as its content is in no way
35; this statement is not removed. Usage by and for commercial
36; irres a license agreement (See http://www.isb-sib.ch/announce/mail-to-license@isb-sib.ch).
37; -----
38; 78; AAP86084.1; .;
39; 0935; SSB; 1.
40; DNA repair; DNA replication; Plasmid.
41; 4 109
42; 38 AA; 20451 MW; B43832FBC232CF4 CRC64;
43; larity 12.9%; Score 78.5; DB 1; Length 188;
44; conservative 33.8%; Pred. No. 0.71;
45; Mismatches 8; Mismatches 30; Indels 13; Gaps 5;
46;
47; HAATTGNSCICRDSGTDSDVTDTQQQAENSAVPTADTRSPQ- RDPVPRPGRG 89
48; ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
49; ASD--GDS-----DSGTRASQSQSPASQASQSAFTGQ-RQPAPRQPAQPPSGFG 161
50;
51; ---PRRKQNVGDL 103
52; |||||
53; EDIPFARPAALDGI 178

STANDARD; PRT; 1483 AA.
39; 095247; 095277;
40; (Rel. 41, Created)
41; (Rel. 41, Last sequence update)
42; (Rel. 41, Last annotation update)
43; adjacent to zinc finger domain protein 1B (Williams-Beuren

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DE syndrome chromosome region 9 protein) (WBSR9) (Williams syndrome
DE transcription factor) (hWALP2).
GN BAZ1B OR WBSR9 OR WBSR10 OR WSTF.
OS Homo sapiens (human)
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
ON NCBI_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=9907764; PubMed=9858827;
RA Peoples R.J., Cisco M.J., Kaplan P., Francke U.;
RT "Identification of the WBSR9 gene, encoding a novel transcripti
RL regulator, in the Williams-Beuren syndrome deletion at 7q11.23."
RN Cytogenet. Cell Genet. 82:238-246(1998).
RN [2]
RN SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=99047530; PubMed=9828126;
RA Lu X., Meng X., Morris C.A., Keating M.T.;
RT "A novel human gene, WSTF, is deleted in Williams Syndrome."
RN Genomics 54:241-249(1998).
RN [3]
RN SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RX TISSUE=Testis;
RN MEDLINE=20130112; PubMed=10662543;
RA Jones M.H., Hamana N., Nezu J., Shimane M.;
RT "A novel family of bromodomain genes."
RN Genomics 63:40-45(2000).
RN [4]
RN SEQUENCE FROM N.A.
RX Minx P., Graves T., Duckels G., Harrison M., Waterston R.;
RN Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [5]
RN FUNCTION.
RX MEDLINE=21977304; PubMed=11980720;
RA Bozhenok L., Wade P.A., Varga-Weisz P.;
RT "WSTF-ISWI chromatin remodeling complex targets heterochromatic
RN replication foci."
RN EMBO J. 21:2231-2241(2002).
CC -!- FUNCTION: Forms a chromatin remodeling complex that mobilize
CC nucleosomes and reconfigures irregular chromatin to a regula
CC nucleosomal array structure.
CC -!- SUBUNIT: Interacts with ISWI (imitation SWI protein) to form
CC WSTF-ISWI chromatin remodeling complex (WICH).
CC -!- SUBCELLULAR LOCATION: Nuclear (Potential). Accumulates in
CC pericentromeric heterochromatin during replication.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q9UGO-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q9UGO-2; Sequence=VSP_000552;
CC -!- TISSUE SPECIFICITY: Ubiquitously expressed with high levels
CC expression in heart, brain, placenta, skeletal muscle and ov
CC -!- DEVELOPMENTAL STAGE: Expressed at equal levels in 19-23 week
CC fetal tissues.
CC -!- DISEASE: Haploinsufficiency of BAZ1B may be the cause of cer
CC cardiovascular and musculo-skeletal abnormalities observed i
CC Williams-Beuren syndrome (WBS), a rare developmental disorde
CC is a contiguous gene deletion syndrome involving genes from
CC chromosome band 7q11.23.
CC -!- SIMILARITY: Belongs to the WAL family.
CC -!- SIMILARITY: Contains 1 bromodomain.
CC -!- SIMILARITY: Contains 1 DDT domain.
CC -!- SIMILARITY: Contains 1 PHD-type zinc finger.
CC -!- SIMILARITY: Contains 1 WAC domain.
CC -!- CAUTION: Ref.2 sequence differs from that shown due to frame
CC in positions 1031, 1042 and 1422.
CC -!- CAUTION: Ref.3 sequence differs from that shown due to a
CC frameshift in position 1478.
CC -!- CAUTION: Ref.4 sequence differs from that shown due to error
CC gene model prediction.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a col.

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3; AAD08675.1; -;
0; AAC97879.1; ALT_FRAME.
3; BAA89210.1; ALT_FRAME.
1; AAD04720.1; ALT_SEQ.
3; -; NOT_ANNOTATED_CDS.
1B91.

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); F: zinc ion binding; N
); P: transcription; NAS.
001487: Bromodomain

PHD; 1.
3; BROMODOMAIN.

1; DDT; 1.
3; PHD; 1.

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)14; BROMODOMAIN_2; 1.
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}59; ZF_PHD_1; 1.
)16; ZF_PHD_2; 1.

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4 668

1426 BROMODOMAIN.

33-586 COILED COIL
33-587 COILED COIL
33-588 COILED COIL

NO	COILED COIL
10	853
15	1292

	Missing (in %)	Total
663		
Missing (in %)		
663		

14	$K \rightarrow N(\overline{N} B)$
14	$K \rightarrow N(\overline{N} B)$

36	K → E (IN R)
36	136

298 Y \rightarrow V (IN R)

1191 R -> P (IN RI

38	1438	A -> V (IN RI
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irility 27.5%; Pred. No. 8;

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1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100

CONTENTS OF THE 107

APPVDDNAEVMELVLOT 1334

FT	260	N-LINKED (GLC/NAC. . .) (POTENTIAL).
SO	286	AA. 28844 MW. D1P4947C68D5805 C8C6C.

Matches 27; Conservative 6; Mismatches 25; Indels 20; G

147 GNGGVQKPNQANKETQNNNSNV-QQDSQTKNSVPPPTQDADTKSPTAQPEQAENSA-P

db 205 TESPELOSAPENKGTQH 222

RESULT 5

AC O00555; P78510; P78511; Q16290; Q92690; Q99790; Q99791; Q99792;
AC Q99793;

DT 10-OCT-2003 (Rel. 42, Last annotation update)

[illegible]

533; PubMed=7540170;
 Ishaashi S., Murakami K., Nakayama K.;
 fic presence of two TGN38 isoforms and absence of TGN41
 1. 270:14471-14476(1995).
 [N.A.
 60; TISSUE=Aorta, and Testis;
 1683; PubMed=12466851;
 Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 Sato N., Sato R., Suzuki H., Yamanaka I., Kiyosawa H.,
 Iru Y., Hasegawa Y., Nogami A., Schonbach C., Gojibori T.,
 Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
 Agani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 Gariboldi M., Gissi C., Godzik A., Gough J.,
 Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 Waji H., Kawasawa Y., Kedzierski R.M., King B.L.,
 Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 Maltais L., Marchionni L., McKenzie L., Miki H.,
 Numata K., Okido T., Pavan W.J., Perlea G., Pesole G.,
 Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 Red J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 Schneider C., Sempie C.A., Setou M., Shimada K.,
 Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 Wagner L., Wahlstedt C., Wang Y., Watanabe Y., Wells C.,
 Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 Zhan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 Iikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 Iaki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 Izume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 Yoshino M., Waterston R., Lander E.S., Rogers J.,
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 length cDNAs.;
 53-573(2002).
 [N.A.
 1257; PubMed=12477932;
 L., Feingold E.A., Grouse L.H., Derge J.G.,
 Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
 Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 Soares M.B., Bonaldo M.P., Casavant T.L., Schetz T.E.,
 J., Uedlin I.B., Toshlyuki S., Carninci P., Prange C.,
 Xuellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 Ton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,
 Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 Touchman J.W., Green E.D., Dickson M.C.,
 Grimwood J., Schmutz J., Myers R.M.,
 S.N., Krzywinski M.I., Skalska U., Smalios D.E.,
 Schein J.E., Jones S.J.M., Marra M.A.;
 and initial analysis of more than 15,000 full-length human
 cDNA sequences.;
 Acad. Sci. U.S.A. 99:16899-16903(2002).
 May be involved in regulating membrane traffic to and
 is-Golgi network.
 AR LOCATION: Type I membrane protein. Primarily in trans-
 work. Cycles between the trans-Golgi network and the cell
 returning via endosomes (By similarity).
 ECIFICITY: Widely expressed.
 EOGUS: Also found in strains BALB/c, C57BL/6 and DBA/2.
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 DR EMBL; D50031; BAA08757.1; -;
 DR EMBL; AK041302; BAC30896.1; -;
 DR EMBL; AK076586; BAC36404.1; -;
 DR EMBL; BC009143; BAA09143.1; -;
 DR PIR; B56940; B56940.
 DR MGI; MGI:105080; Tgln1.
 KW Signal; Transmembrane; Glycoprotein; Repeat; Golgi stack.
 FT SIGNAL 1 17
 FT CHAIN 18 353
 FT TRANS-GOLGI NETWORK INTEGRAL MEMBR
 FT PROTEIN 1.
 FT EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 18 298
 FT TRANSMEM 299 319
 FT DOMAIN 320 353
 FT SITE 346 349
 FT CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 131 178
 FT ENDOCYTOSIS SIGNAL (BY SIMILARITY).
 FT REPEAT 131 138
 FT 6 X 8 AA TANDEM REPEATS.
 FT REPEAT 139 146
 FT 1.
 FT REPEAT 147 154
 FT 2.
 FT REPEAT 155 162
 FT 3.
 FT REPEAT 163 170
 FT 4.
 FT REPEAT 171 178
 FT 5.
 FT CARBOHYD 110 110
 FT N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 293 293
 FT N-LINKED (GLCNAC. .) (POTENTIAL).
 SQ SEQUENCE 353 AA; 37848 MW; 95C340C2FA421EB3 CRC64;
 Query Match 12.0%; Score 73; DB 1; Length 353;
 Best Local Similarity 30.5%; Pred. No. 5.1;
 Matches 18; Conservative 9; Mismatches 28; Indels 4;
 QY 32 GFGGAATTGNSICRDSDSDTQQAENSAPVADTFRSQRDVRPRR;
 Db 148 GDSGKPTAGSNKATDSDSGSKTKVDLDRPSKIS----PDFTSKTDKVPTEK
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 CA13 HUMAN
 ID CA13 HUMAN STANDARD; PRT; 1466 AA.
 AC P02461; Q15112;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Collagen alpha 1(III) chain precursor.
 GN COL3A1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skin fibroblast;
 RX MEDLINE=89350838; PubMed=2764886;
 RA Ala-Kokko L., Kontusaari S., Baldwin C.T., Kuivaniemi H.,
 Prockop D.J.;
 RT "Structure of cDNA clones coding for the entire prepro alpha 1 (C
 RT chain of human type III procollagen. Differences in protein stru
 RT from type I procollagen and conservation of codon preferences.";
 RL Biochem. J. 260:509-516(1989).
 RN [2]
 RP SEQUENCE OF 149-1225 FROM N.A.
 RX MEDLINE=89386015; PubMed=2780304;
 RA Janeczko R.A., Ramirez F.;
 RT "Nucleotide and amino acid sequences of the entire human alpha 1
 RT (III) collagen.";
 RL Nucleic Acids Res. 17:6742-6742(1989).
 RN [3]
 RP SEQUENCE OF 168-398.
 RX MEDLINE=7134724; PubMed=557335;
 RA Seyer J.M., Kang A.H.;
 RT "Covalent structure of collagen: amino acid sequence of cyanogen

FT	SIGNAL	1	20	POTENTIAL.
FT	CHAIN	21	238	MEROZOITE SURFACE ANTIGEN 2.
FT	PROPEP	239	262	HYDROPHOBIC, REMOVED DURING MATURATION (BY SIMILARITY).
FT	DOMAIN	44	188	POLYMORPHIC REGION.
FT	DOMAIN	91	98	POLY-THR.
FT	CARBOHYD	22	22	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	36	36	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	139	139	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	211	211	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	235	235	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	236	236	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	SEQUENCE	262 AA;	27374 MW;	72E0B2A315E9D154 CRC64;
Query Match				
Best Local Similarity		11.9%; Score 72.5; DB 1; Length 262;		
Matches		Pred. No. 4.1; Mimatches 6; Indels 13;		
Matches 24; Conservative				
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Db	137	TQNNSNV-QQDSQTKSNVPPTQADTKSPA	QEQAEASA-PTAQTESPELQSA	
QY	88	RGPH 91		
Db	195	TGQH :98		
RESULT 10				
MSA2 PLAF7				
ID	MSA2 PLAF7	STANDARD;	PRT;	272 AA.
AC	F50498;			
DT	01-OCT-1996	(Rel. 34, Created)		
DT	01-OCT-1996	(Rel. 34, Last sequence update)		
DT	01-OCT-1996	(Rel. 34, Last annotation update)		
DE	Merozoite surface antigen 2 precursor (MSA-2) (45 kDa merozoite surface antigen).			
GN	MSA2.			
OS	Plasmodium falciparum (isolate 3D7).			
OC	Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.			
OX	NCBI_TaxID=36329;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=90205972; PubMed=2181307;			
RA	Smeyne J.A., Peterson M.G., Coppel R.L., Saul A.J., Kemp D.J., Anders R.F.;			
RA	"Structural diversity in the 45-kilodalton merozoite surface ant of Plasmodium falciparum."			
RT	Mol. Biochem. Parasitol. 39:227-234(1990).			
RL	-!- FUNCTION: May play a role in the merozoite attachment to the erythrocyte.			
CC	-!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anch (Potential).			
CC	-!- DEVELOPMENTAL STAGE: During the trophozoite and schizont sta			
CC	This SWISS-PROT entry is copyright. It is produced through a col between the Swiss Institute of Bioinformatics and the EMBL ou the European Bioinformatics Institute. There are no restriction use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib.ch or send an email to license@isb-sib.ch).			
CC	EMBL; M28891; AAA29686.1; -			
DR	InterPro; IPE001136; MSA_2.			
DR	Pfam; PF00985; MSA_2; 1.			
KW	Malaria; Membrane; Glycoprotein; Antigen; Signal; Repeat;			
KW	GPI-anchor; Merozoite.			
FT	SIGNAL	1	20	POTENTIAL.
FT	CHAIN	21	248	MEROZOITE SURFACE ANTIGEN 2.
FT	PROPEP	249	272	HYDROPHOBIC, REMOVED DURING MATURATION (BY SIMILARITY).
FT	DOMAIN	44	198	POLYMORPHIC REGION.
FT	DOMAIN	95	108	POLY-THR.

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1 N-LINKED (GLCNAC. . ) (POTENTIAL).
2 N-LINKED (GLCNAC. . ) (POTENTIAL).
3 N-LINKED (GLCNAC. . ) (POTENTIAL).
4 N-LINKED (GLCNAC. . ) (POTENTIAL).
5 N-LINKED (GLCNAC. . ) (POTENTIAL).
6 N-LINKED (GLCNAC. . ) (POTENTIAL).
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9 AA; 27971 MW; 9D9CF223BF2B483D CRC64;
10 11.9%; Score 72.5; DB 1; Length 272;
11 Identity 37.5%; Pred. No. 4.3;
12 Descriptive 6; Mismatches 21; Indels 13; Gaps 4
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14 C1CRDDSGTDSV-----DT-----QQQAENSVPATDTRSQPDVPPRRG 87
15 WV-QQDSQTKSNVPTQDATKSFTAQPEQAENSA-PTAEQTSPQLQSAPENKG 204
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21 STANDARD; PRT; 274 AA.
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24 31. 34, Last sequence update)
25 31. 34, Last annotation update)
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99 31. 34, Last annotation update)
100 31. 34, Last annotation update)

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FT	CARBOHYD	249	249	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	273	273	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	274	274	N-LINKED (GLCNAC. . .) (POTENTIAL).
SEQ	SEQUENCE	300 AA;	30131 MW; A01E17D36075D7D6 CRC64;	
Query Match				
	Best Local Similarity	37.58;	Score 72.5; DB 1; Length 300;	
	Matches	24; Conservative	6; Mismatches	21; Indels
				13; G
QY	39	TMGNSCI	CRDSDSGDSDV-----DT-----	QQQAENSAVETADTRSQRPDPVRF
Db	175	TQNSNV-QQDSQTKSNVPTQDADTKSP	TAQPEQAENSA-PTAQTESPELQSAF	
QY	88	RGPH	91	
Db	233	TQGH	236	
RESULT 14				
MSA2_PLAFZ				
ID	MSA2_PLAFZ	STANDARD;	PRT;	300 AA.
AC	Q03645;			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DT	01-OCT-1996 (Rel. 34, Last annotation update)			
GN	MSA2.			
OS	Plasmodium falciparum (isolate mad71 / Papua New Guinea).			
OC	Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.			
OX	NCBI_TaxID=70154;			
RP	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=91156685; PubMed=2000383;			
RA	Smylethe J.A., Coppel R.L., Day K.P., Martin R.K., Oduola A.M.J.,			
RA	Kemp D.J., Anders R.F.;			
RT	"Structural diversity in the Plasmodium falciparum merozoite surf-			
RT	antigen 2.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 88:1751-1755(1991).			
CC	!- FUNCTION: May play a role in the merozoite attachment to the			
CC	erythrocyte.			
CC	SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anch			
CC	(Potential).			
CC	!- DEVELOPMENTAL STAGE: During the trophozoite and schizont stag			
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CC	entities requires a license agreement (see http://www.isb-sib.ch).			
CC	or send an email to license@isb-sib.ch .			
CC	EMBL; M59768; AAA29696.1; -			
DR	PIR; A39112; A39112.			
DR	InterPro; IPR001136; MSA_2.			
DR	Pfam; PF00985; MSA_2; 1.			
KW	Malaria; Membrane; Glycoprotein; Antigen; Signal; Repeat;			
KW	GPI-anchor; Merozoite.			
FT	SIGNAL	1	20	POTENTIAL.
FT	CHAIN	21	276	MEROZOITE SURFACE ANTIGEN 2.
FT	PROPEP	277	300	HEROZOITOPHIC, REMOVED DURING MATURATION
FT				(BY SIMILARITY).
FT	DOMAIN	44	226	POLYMORPHIC REGION.
FT	DOMAIN	129	136	POLY-THR.
FT	CARBOHYD	22	22	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	36	36	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	177	177	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	249	249	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	273	273	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	274	274	N-LINKED (GLCNAC. . .) (POTENTIAL).
SEQ	SEQUENCE	300 AA;	30101 MW; E4116107747AA10D CRC64;	
Query Match				
	Best Local Similarity	37.58;	Score 72.5; DB 1; Length 300;	

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in search, using sw model

ril 2, 2004, 10:21:14 ; Search time 39 Seconds
(without alignments)
946.555 Million cell updates/sec

-10-066-273-9

MIVEGNAVFASRLGQGLL.....QNVDELDTLAVIRTLVDK 117

OSUM62

pop 10.0 , Gapext 0.5

17041 seqs, 315518202 residues

ts satisfying chosen parameters: 1017041

gth: 0

inimum Match 0%

aximum Match 100%

isting first 45 summaries

PTREMBL 25:*

sp_archea:*

sp_bacteria:*

sp_fungi:*

sp_human:*

sp_invertebrate:*

sp_mammal:*

sp_mhc:*

sp_organelle:*

sp_phase:*

sp_plant:*

sp_rodent:*

sp_virus:*

sp_vertebrate:*

sp_unclassified:*

sp_rvirus:*

sp_bacteriap:*

sp_archeap:*

the number of results predicted by chance to have a
than or equal to the score of the result being printed,
ed by analysis of the total score distribution.

SUMMARIES

seq	Length	DB	ID	Description
3.2	576	4	Q96DX4	Q96dx4 homo sapien
3.2	576	6	Q95LP3	Q95lp3 macaca fasc
3.1	117	11	Q8BLS8	Q8b1s8 mus musculus
1.3	576	11	Q8C039	Q8c039 mus musculus
1.3	576	11	Q8BVR6	Q8bvr6 mus musculus
1.1	601	16	Q82F17	Q82fi7 streptomyce
4.0	290	5	Q20394	Q20394 caenorhabdi
3.1	356	10	Q9ATR4	Q9atr4 oryza sativ
3.1	388	10	Q94IM8	Q94im8 oryza sativ
3.1	388	10	Q8LNM8	Q8lnm8 oryza sativ
3.1	388	10	Q7YIX7	Q7yix7 oryza sativ
3.1	5146	5	Q9VXR3	Q9vix3 drosophila
3.0	970	10	Q9AYF2	Q9ayf2 oryza sativ
2.9	188	2	Q7XF23	Q7xf23 oryza sativ
2.9	188	2	Q7WX07	Q7wx07 alcaigenes
2.8	179	5	Q9XZ40	Q9xz40 plasmodium

17	78	12.8	191	5	Q9U0C1	Q9u0c1 pla:
18	78	12.8	203	5	Q9U0C0	Q9u0c0 pla:
19	78	12.8	480	5	Q27033	Q27033 the:
20	77.5	12.7	550	12	Q40912	Q40912 kai
21	77.5	12.7	550	12	F88903	F88903 kai
22	76.5	12.6	634	4	Q8IXW0	Q8ixw0 homc
23	76	12.5	1063	16	Q8XXH5	Q8xxh5 ra:
24	75.5	12.4	948	5	Q9U304	Q9u304 caer
25	75	12.3	147	5	O15805	O15805 pla:
26	75	12.3	183	5	Q9U0B5	Q9u0b5 pla:
27	75	12.3	183	5	Q9U0B6	Q9u0b6 pla:
28	75	12.3	204	5	Q9U0B4	Q9u0b4 pla:
29	75	12.3	260	5	Q8IT83	Q8it83 pla:
30	75	12.3	267	13	Q9PUV0	Q9puv0 bal
31	75	12.3	278	5	Q25862	Q25862 pla:
32	75	12.3	291	5	Q25789	Q25789 pla:
33	74.5	12.2	121	12	Q8QRK4	Q8qrk4 hei
34	74.5	12.2	462	3	Q42721	Q42721 peni
35	74.5	12.2	2120	5	Q8IAK1	Q8iak1 pla:
36	74	12.2	850	16	Q8FML9	Q8fml9 coi
37	73.5	12.1	416	12	Q81265	Q81265 her
38	73	12.0	206	5	Q9U0C3	Q9u0c3 pla:
39	73	12.0	220	5	Q9U0B3	Q9u0b3 pla:
40	73	12.0	222	5	Q9U0B1	Q9u0b1 pla:
41	73	12.0	353	11	Q62313	Q62313 mu:
42	73	12.0	579	2	Q8GFF2	Q8gff2 stre
43	73	12.0	1160	5	Q8T0V9	Q8t0v9 droe
44	73	12.0	1163	4	Q8N6U4	Q8n6u4 homc
45	73	12.0	3571	10	Q9SL27	Q9sl27 are

ALIGNMENTS

RESULT 1

Q96DX4	PRELIMINARY;	PRT;	576 AA.
ID	Q96DX4		
AC	Q96DX4;		
DT	01-DEC-2001 (TREMBLrel. 19, Created)		
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)		
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)		
DE	Hypothetical protein KIAA1972.		
GN	KIAA1972.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Lymph;		
RA	Strausberg R.;		
RL	Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Brain;		
RX	MEDLINE=21842142; PubMed=11853119;		
RA	Nagase T., Kikuno R., Ohara O.;		
RT	"Prediction of the coding sequences of unidentified human genes.		
RT	The complete sequences of 50 new cDNA clones which code for large		
RL	DNA res. 8:319-327(2001).		
DR	EMBL; BC013173; AAH13173.1; -		
DR	EMBL; AB075852; BAB85558.1; -		
DR	InterPro; IPR008938; ARM.		
DR	InterPro; IPR003877; SPRY receptor.		
DR	InterPro; IPR001841; Znf_ring.		
DR	Pfam; PF00622; SPRY; 1.		
DR	SMART; SM00184; RING; 1.		
DR	SMART; SM00449; SPRY; 1.		
DR	PROSITE; PS50089; ZF_RING_2; 1.		
KN	Hypothetical protein.		
SEQUENCE	576 AA; 64180 MW; 8598E43E96691F9B CRC64;		

99.2%; Score 604; DB 4; Length 576;
arity 100.0%; Pred. No. 1.2e-57;
conservative 0; Mismatches 0; Indels 0; Gaps 0;

GWAVFLASRLGQGLLLTLEEHIAHFLGTGGAATMGNSCICRDSGTDSDVDTQQ 60
|||||
GWAVFLASRLGQGLLLTLEEHIAHFLGTGGAATMGNSCICRDSGTDSDVDTQQ 60
|||||

NSAVPTADTRSPQRPDPVPPRRGPGHPHPRKKQNVGLVLDLTLAVIRTLVD 116
|||||
NSAVPTADTRSPQRPDPVPPRRGPGHPHPRKKQNVGLVLDLTLAVIRTLVD 116
|||||

RELIMINARY; PRT; 576 AA.

TREMBLrel. 19, Created)
TREMBLrel. 19, Last sequence update)
TREMBLrel. 25, Last annotation update)
protein.
ularis (Crab eating macaque) (Cynomolgus monkey).
tazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
heria; Primates; Catarrhini; Cercopitheidae;
ae; Macaca.
41;

N.A.
; Osada N., Hida M., Kusuda J., Tanuma R., Hirai M.,
ano S.;
novel full-length cDNA clones from macaque testis cDNA
T-2001) to the EMBL/GenBank/DBJ databases.
5; BAB69714.1; -
008938; ARM.
003877; SPRY_receptor.
001841; Znf_ring.
; SPRY; 1.
4; RING; 1.
9; SPRY; 1.
089; ZF_RING_2; 1.
protein.
6 AA; 64259 MW; 68D230AD1C4F5F8D CRC64;
arity 96.2%; Score 586; DB 6; Length 576;
conservative 0; Mismatches 3; Indels 0; Gaps 0;

GWAVFLASRLGQGLLLTLEEHIAHFLGTGGAATMGNSCICRDSGTDSDVDTQQ 60
|||||
GWAVFLASRLGQGLLLTLEEHIAHFLGTGGAATMGNSCICRDSGTDSDVDTQQ 60
|||||

NSAVPTADTRSPQRPDPVPPRRGPGHPHPRKKQNVGLVLDLTLAVIRTLVD 116
|||||
NSAVPTADTRSPQRPDPVPPRRGPGHPHPRKKQNVGLVLDLTLAVIRTLVD 116
|||||

RELIMINARY; PRT; 117 AA.

TREMBLrel. 23, Created)
TREMBLrel. 23, Last sequence update)
TREMBLrel. 23, Last annotation update)
Spla and the Ryanodine receptor.
(Mouse).
tazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
heria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
090;

N.A.
6J; TISSUE=Cortex;

RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotati
60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK043522; BAC31566.1; -.
KW Hypothetical protein.
SQ SEQUENCE 117 AA; 12738 MW; D3FEC471ABD55D3C CRC64;

Query Match 92.1%; Score 561; DB 11; Length 117;
Best Local Similarity 91.5%; Pred. No. 9.5e-54;
Matches 107; Conservative 3; Mismatches 7; Indels 0; C

QY 1 MIVFGWAVFLASRLGQGLLLTLEEHIAHFLGTGGAATMGNSCICRDSGTDSDV
|||||
DB 1 MIVFGWAVFLASRLGQGLLLTLEEHIAHFLGTGGAATMGNSCICRDSGAE
|||||

QY 61 QQAENSAPVPTADTRSPQRPDPVPPRRGPGHPHPRKKQNVGLVLDLTLAVIRTLV
|||||
DB 61 QQAENSAPVPTADTRSPQRPDPVPPRRGPGHPHPRKKQNVGLVLDLTLAVIRTLV
|||||

RESULT 4
Q8C039 PRELIMINARY; PRT; 576 AA.
ID Q8C039;
AC Q8C039;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Hypothetical Sp1a and the Ryanodine receptor.
GN 4930470D19RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
OX NCBI_taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotati
60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK032416; BAC27858.1; -.
DR MGD; MGI:1914860; 4930470D19RIK.
DR InterPro; IPR008938; ARM.
DR InterPro; IPR008977; SPRY_receptor.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00622; SPRY; 1.
DR SMART; SM00184; RING; 1.
DR SMART; SM00449; SPRY; 1.
DR PROSITE; PS00089; ZF_RING_2; 1.
KW Hypothetical protein.
SQ SEQUENCE 576 AA; 64340 MW; D72D60E803911D02 CRC64;

Query Match 91.3%; Score 556; DB 11; Length 576;
Best Local Similarity 91.4%; Pred. No. 2.2e-52;
Matches 106; Conservative 3; Mismatches 7; Indels 0; C

QY 1 MIVFGWAVFLASRLGQGLLLTLEEHIAHFLGTGGAATMGNSCICRDSGTDSDV
|||||
DB 1 MIVFGWAVFLASRLGQGLLLTLEEHIAHFLGTGGAATMGNSCICRDSGAE
|||||

QY 61 QQAENSAPVPTADTRSPQRPDPVPPRRGPGHPHPRKKQNVGLVLDLTLAVIRTLV
|||||
DB 61 QQAENSAPVPTADTRSPQRPDPVPPRRGPGHPHPRKKQNVGLVLDLTLAVIRTLV
|||||

RESULT 5
Q8BVR6 PRELIMINARY; PRT; 576 AA.
ID Q8BVR6

TrEMBLrel. 23, Last sequence update)
 TrEMBLrel. 25, Last annotation update)
 F1a and the Ryanodine receptor (Hypothetical
 Mouse).
 azoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 eria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
)90;
 N.A.
 J; Tissue=Testis;
 83; PubMed=12466851;
 isortium,
 me Exploration Research Group Phase I & II Team;
 he mouse transcriptome based on functional annotation of
 ngth cDNAs.",
 1-573(2002).
 N.A.
 57; PubMed=12477932;
 ., Feingold E.A., Grouse L.H., Derge J.G.,
 Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
 Jordan H., Moore T., Max S.I., Wang J., Heien F.,
 Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 f., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
 nellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 Swan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 on E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 dan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 Touchman J.W., Green E.D., Dickson M.C.,
 Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 ., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
 irra M.A.;
 id initial analysis of more than 15,000 full-length human
 sequences.",
 ad. Sci. U.S.A. 99:16899-16903(2002).
 N.A.
 1-2003) to the EMBL/GenBank/DBJ databases.
); BAC36485.1; -.
 .; AAH54121.1; -.
 860; 4930470D19rik.
 08938; ARM.
 03877; SPRY_receptor.
 01841; Znf_ring.
 . SPRY; 1.
 .; RING; 1.
 .; SPRY; 1.
 189; Zf_RING 2; 1.
 rotein.
 5 AA; 64322 MW; 823C3532FCE18387 CRC64;
 91.3%; Score 556; DB 11; Length 576;
 arity 91.4%; Pred. No. 2.2e-52;
 nservative 3; Mismatches 7; Indels 0; Gaps 0;
 3WAVFLASRLGQGLLTLEEHIAHFLGTGGAATTMGNSICRDSGTDSDSDVDTQ 60
 |||||
 3WAVFLASRLGQGLLTLEEHIAHFLGTGATATMGNSICRDSGDAENVDTQ 60
 |||||
 3WAVPTADTSQRDPVPRPRRGPHPRKQNVQDGLVLDTLAVIRTLVD 116
 |||||
 3WVPTADSRSPRDPVPRPRRGPHPRKQNVQDGLVLDTLAVIRTLVD 116
 |||||

RESULT 6
 Q82FI7
 ID Q82FI7 PRELIMINARY; PRT; 601 AA.
 AC Q82FI7;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Putative thiamine biosynthesis protein.
 GN THIA OR SAV4265.
 OS Streptomyces avermitilis.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=33903;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
 RX MEDLINE=21477403; PubMed=11572948;
 RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
 Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,
 RA Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
 RT "Genome sequence of an industrial microorganism Streptomyces
 RT avermitilis: deducing the ability of producing secondary
 RT metabolites.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
 RX MEDLINE=22608306; PubMed=12692562;
 RA Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba
 RA Sakaki Y., Hattori M., Omura S.;
 RT "Complete genome sequence and comparative analysis of the industr
 RT microorganism Streptomyces avermitilis.";
 RL Nat. Biotechnol. 21:526-531(2003).
 DR EMBL; AP005038; BAC71977.1; -.
 DR GO; GO:0009228; P:thiamin biosynthesis; IEA.
 DR InterPro; IPR002817; Thic.
 DR Pfam; PF01964; Thic; 1.
 DR ProDom; PD007048; Thic; 1.
 DR TIGRFAMS; TIGR00190; Thic; 1.
 DR Complete proteome.
 SQ SEQUENCE 601 AA; 66485 MW; B149CD75A602FCF5 CRC64;
 Query Match 14.1%; Score 86; DB 16; Length 601;
 Best Local Similarity 32.3%; Pred. No. 0.86; Mismatches 22; G
 Matches 31; Conservative 7;
 QY 39 TMGNSICRDSG--TDDSVDTQQA-----ENSAVPTADTSQRDPVPR-----
 DB 55 TNGESVLYDTSGPYTDPSTVDRGLAPLRNWIARGDTTEYAGRPVRPDDG
 QY 84 -PRRG-----PHEPRKKQNVQDGLVLDTLAVIR 112
 DB 115 SPRGGLNLDVAFPRGPRGPRGRDQGAQTAYAR 150
 RESULT 7
 Q20394
 ID Q20394 PRELIMINARY; PRT; 290 AA.
 AC Q20394;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE F44D12.6 protein.
 GN F44D12.6.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoid
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Coles L.;


```

13.14; Score 79.5; DB 10; Length 388;
urity 32.34; Pred. No. 2.7;
nservative 6; Mismatches 27; Indels 9; Gaps 1;
DDSGTDDSDVDTQQQAENSA-----VPTADTRSQRPDPVPRPRGRGHPHEP 93
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
EDGSSSLSDGKQQQHSNADPRGGGAGDHKGAAHGSDGKPAKPRRAANPKPP 238
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
0
0
ELIMINARY; PRT; 388 AA.
EMBLrel. 25, Created)
EMBLrel. 25, Last sequence update)
EMBLrel. 25, Last annotation update)
ding 1.
indica cultivar-group).
diplanctae; Streptophyta; Embryophyta; Tracheophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae;
Oryzaceae; Oryza.
46;
N.A.
36;
Zhao Z., Zhao Y., Sun C.R., Luo D.;
al and expression analysis of Ost1 in rice.";
2-2003) to the EMBL/GenBank/DBJ databases.
; AAP37176.1; -
; AA; 41504 MW; 8CF363D2EAA02743 CRC64;
13.14; Score 79.5; DB 10; Length 388;
urity 32.34; Pred. No. 2.7;
nservative 6; Mismatches 27; Indels 9; Gaps 1;
DDSGTDDSDVDTQQQAENSA-----VPTADTRSQRPDPVPRPRGRGHPHEP 93
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
EDGSSSLSDGKQQQHSNADPRGGGAGDHKGAAHGSDGKPAKPRRAANPKPP 238
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
5
10
ELIMINARY; PRT; 5146 AA.
EMBLrel. 13, Created)
EMBLrel. 22, Last sequence update)
EMBLrel. 25, Last annotation update)
1.
anogaster (Fruit fly).
azoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Pterygota; Diptera; Brachycera; Muscomorpha;
Drosophilidae; Drosophila.
27;
N.A.
ay;
006; PubMed=10731132;
alniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
3...Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Kortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Rogers Y.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,
le C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

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RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M
RA Beeson K.Y., Banos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Borchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dun
RA Durbin K.J., Evangelista C.C., Fertaz C., Ferreira S., Fleischman
RA Fosler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., McPherson D.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Stupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [2]
RN SEQUENCE FROM N.A.
RA Celniker S.E., Adams M.D., Krommiller B., Wan K.H., Holt R.A.,
RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y
RA Banzon J., An H., Baldwin J., Beeson K.Y., Busam D.A.,
RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
RA Ferreira S., Frise E., Galle R.F., Garg N.S., George R.A.,
RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
RA Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J
RA Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,
RA Phouenavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
RA Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,
RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
RT "Sequencing of Drosophila melanogaster genome.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RN SEQUENCE FROM N.A.
RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell
RA Hradecky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,
RA Tupy J.L., Bergman Y., Berman B., Carlson J.W., Celniker S.E.,
RA Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
RA Krommiller B., Marshall B., Millburn G., Richter J., Russo S.,
RA Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
RT "Annotation of Drosophila melanogaster genome.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RN SEQUENCE FROM N.A.
RA Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RN SEQUENCE FROM N.A.
RA FlyBase;
RA Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL: AE003500; AAP48495.2; -
DR FlyBase; FBgn0030674; CG8184.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0005743; C:mitochondrial inner membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.

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DR GO; GO:0006310; P-DNA recombination; IEA.
GO; GO:0006508; P-procaryotic translation; IEA.
DR InterPro; IPROO0209; Peptidase S8.
DR InterPro; IPROO1584; Rve.
DR Pfam; PF00665; rve; 1.
DR PROSITE; PS00136; SUBTILASE ASP.; 1.
DR SEQUENCE 970 AA; 108499 MW; 14D8F3EB056B194A CRC64;
SQ

Query Match 13.0%; Score 79; DB 10; Length 970;
Best Local Similarity 27.4%; Pred. No. 8.8;
Matches 31; Conservative 12; Mismatches 42; Indels 28; C

```

QY      4  FGWAVFIARSLG---QGLLTLLEHIAHFVGT-----GGAATTM--GNSC]
      : | | : : | | : | | : | | : | | : | | : | | : | |
      : | | : : | | : | | : | | : | | : | | : | | : | |
Db      551 YSWVFFNATKDEAFQHRGULFDL---LEFFGSLKRIKSDNGGTLQVQGEDSC]

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Qy 50 SGTDDSDVTQQQQAENSAVPTADTFSQPRDPVPRRRGRGHEPRRKKQNVDG 10

Dh 608 SDQDDDDKVSAGOTGROAGOTAST-----PP--GRPDERSNRRPGSSG 64

DD DD SUUUUUUAVSAGGUGKQAGQIASI-----PP--GRFFQDEKNRFGSSG G
RESULT 14
QYXF23
ID Q7XF23 PRELIMINARY: PRT: 970 AA.

AD	Q7AFX23	PRELIMINARY; 370 AA.
IC	Q7XF23	
DD	Q7XF23	
DT	01-OCT-2003 (TrEMBLrel. 25, Created)	
DT	01-OCT-2003 (TrEMBLrel. 25, Last sequence update)	
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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STRAIN=cv. Nipponbare;
The Rice Chromosome 10 Sequencing Consortium;
"In-depth view of structure, activity, and evolution of rice
chromosome 10.";
Science 300:1566-1569(2003).

Q12: Sequence 300:1568-1593(1200537).
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 RC STEALING, Nipponbare;
 RC Buell C.R., Wing R.A., McCombie W.R., Messing J., Yuan Q.;
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 RL EMBL, AE017089; AAP53536.1; -.
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DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative single-strand binding protein.

DEPARTMENT OF THE ARMY
OFFICE OF THE CHIEF OF STAFF
WASHINGTON, D. C. 20315

15 2: Fubiquitin-protein ligase activity; IEA.
 16 0; P.transpart; IEA.
 17 2: Pubiquitin cycle; IEA.
 18 008938; ARM.
 19 000589; HECT domain.
 20 001993; Mitoch carrier.
 21 000449; UBA domain.
 22 004170; WWE_dom.

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T-EMBLRel_25, Last annotation update)
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ah R.S., Miller B., Kirchoff K.A., King L., Toth K.,
A Dedhia N.N. McCombie W.P.
1 N.A.
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A Dedhia N.N. McCombie W.P.

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2. Center For Oryza sativa, Nipponbare strain, Chromosome X,
3. "094J09, complete sequence";
4. (G-2000) to the EMBL/GenBank/DBJ databases.

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P-2000) to the EMBL/GenBank/DBJ databases.

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ah R.S., Miller B., Kirchoff K.A., King L., Toth K.

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9; F:subtilase activity; IEA.

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

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aximum Match 100%

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2.3	1531	4	US-09-418-710-29	Sequence 29, Appl
2.3	433	2	US-08-466-120-2	Sequence 2, Appl
2.3	433	5	PCT-US94-07266-2	Sequence 2, Appl
2.3	1525	4	US-09-418-710-69	Sequence 69, Appl
2.2	462	2	US-08-865-597A-2	Sequence 2, Appl
2.1	2509	2	US-08-149-097D-35	Sequence 35, Appl
2.0	623	3	US-09-029-348-3	Sequence 3, Appl
2.0	626	3	US-09-029-348-2	Sequence 2, Appl
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1.7	562	4	US-09-252-991A-20178	Sequence 20178, A
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1.7	863	4	US-09-252-991A-26099	Sequence 26099, A
1.5	396	4	US-09-252-991A-32927	Sequence 32927, A
1.3	191	2	US-08-290-665A-198	Sequence 198, App
1.3	191	2	US-08-290-665A-199	Sequence 199, App
1.3	191	2	US-08-290-665A-200	Sequence 200, App
1.3	191	2	US-08-290-665A-201	Sequence 201, App
1.3	191	2	US-08-290-665A-202	Sequence 202, App
1.3	191	2	US-08-290-665A-203	Sequence 203, App
1.3	191	5	PCT-US95-10398-198	Sequence 198, App
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ALIGNMENTS

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; Sequence 20180, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 20180
; LENGTH: 460
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-20180

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; Sequence 30267, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27

Байлал

Patent No. 5874236
GENERAL INFORMATION:
APPLICANT: Harpold, Michael

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;   OTHER INFORMATION: /product= "AlphaA-1 subunit of
;   OTHER INFORMATION: human calcium channel."
US-08-149-097D-35

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; Sequence 3, Application US/09029348
; Patent No. 6171827
; GENERAL INFORMATION:
; APPLICANT: THE VICTORIA UNIVERSITY OF MANCHESTER
; TITLE OF INVENTION: NOVEL PROCOLLAGENS
; FILE REFERENCE: d087857PUS LISTING
; CURRENT APPLICATION NUMBER: US/09/029,348
; CURRENT FILING DATE: 1998-05-07
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US-09-029-348-3

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; Patent No. 6171827
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; APPLICANT: THE VICTORIA UNIVERSITY OF MANCHESTER
; TITLE OF INVENTION: NOVEL PROCOLLAGENS
; FILE REFERENCE: d087857PUS LISTING
; CURRENT APPLICATION NUMBER: US/09/029,348
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ALIGNMENTS

PRIOR APPLICATION NUMBER: 60/03

; AFFILIATION: WOOD, WILLIAM I.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nuc:
 ; TITLE OF INVENTION: Acids Encoding the Same

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US-10-081-056-6

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lication US/10066500

US20020177165A1

ION:

J. Ahkenazi

Lin P. Baker

Mid A. Botstein

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ION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
ACIDS ENCODING THE SAME

P3130RIC7

TION NUMBER: US/10/066,500

DATE: 2002-02-01

ON NUMBER: 10/002,796

TE: 2001-11-15

ON NUMBER: 60/056974

TE: 1997-08-26

ON NUMBER: 60/059115

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; Publication NO. US20030032057A1
; GENERAL INFORMATION:
; APPLICANT: Avi J. Ashkenazi
; APPLICANT: Kevin P. Baker
; APPLICANT: David A. Botstein
; APPLICANT: Luc Desnoyers
; APPLICANT: Dan L. Eaton
; APPLICANT: Napoleone Ferrara
; APPLICANT: Sherman Fong
; APPLICANT: Wei-Qiang Gao
; APPLICANT: Hanspeter Gerber
; APPLICANT: Mary E. Gerritsen
; APPLICANT: Audrey Goddard
; APPLICANT: Paul J. Godowski
; APPLICANT: Austin L. Gurney
; APPLICANT: Ivar J. Kljavin
; APPLICANT: Jennie P. Mather
; APPLICANT: Mary A. Napier
; APPLICANT: James Pan
; APPLICANT: Nicholas F. Paoni
; APPLICANT: Margaret Ann Roy
; APPLICANT: Timothy A. Stewart
; APPLICANT: Daniel Tumas
; APPLICANT: Colin K. Watanabe
; APPLICANT: P. Mickey Williams
; APPLICANT: William I. Wood
; APPLICANT: Zemin Zang
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUC
; FILE REFERENCE: P3130R1C1
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US2003032062A1

ION:

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P3130R1C2

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ATE: 1999-09-15
ION NUMBER: PCT/US99/21547

100.0%; Score 609; DB 14; Length 117;
arity 100.0%; Pred.No. 1.7e-58;
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US-10-066-494-9
; Sequence 9, Application US/10066494
; Publication No. US20030032063A1
; GENERAL INFORMATION:
; APPLICANT: Avi J. Ashkenazi
; APPLICANT: Kevin P. Baker
; APPLICANT: David A. Botstein
; APPLICANT: Luc Desnoyers
; APPLICANT: Dan L. Eaton
; APPLICANT: Napoleone Ferrara
; APPLICANT: Sherman Fong
; APPLICANT: Wei-Qiang Gao
; APPLICANT: Hanspeter Gerber
; APPLICANT: Mary E. Gerritsen
; APPLICANT: Audrey Goddard
; APPLICANT: Paul J. Godowski
; APPLICANT: Austin L. Gurney
; APPLICANT: Ivar J. Kljavin
; APPLICANT: Jennie P. Mather
; APPLICANT: Mary A. Napier
; APPLICANT: James Pan
; APPLICANT: Nicholas F. Paoni
; APPLICANT: Margaret Ann Roy
; APPLICANT: Timothy A. Stewart
; APPLICANT: Daniel Tumas
; APPLICANT: Colin K. Watanabe
; APPLICANT: P. Mickey Williams
; APPLICANT: William I. Wood
; APPLICANT: Zemin Zang
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NU
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3130RIC9
; CURRENT APPLICATION NUMBER: US/10/066,494
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 10/002,796
; PRIOR FILING DATE: 2001-11-15
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Query Match 100.0%; Score 609; DB 14; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.7e-58;
Matches 117; Conservative 0; Mismatches 0; Indels 0; G

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US-10-066-269-9
; Sequence 9, Application US/10066269
; Publication No. US20030040014A1

TION:

J. Ashkenazi
vin P. Baker
vid A. Botstein
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L. Eaton
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frey Goddard
stin L. Gurney
ar J. Kljavin
mie P. Mather
cy A. Napier
res Pan
holas F. Paoni
garet Ann Roy
nothy A. Stewart
iel Tumas
lin K. Watanabe
lickey Williams
lham I. Wood
nin Zang

ION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
ION: ACIDS ENCODING THE SAME

: P3130R1C4

ATION NUMBER: US/10/066,269

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PRIOR FILING DATE: 1999-11-10
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 TE: 2001-05-30
 ON NUMBER: 09/872035
 TE: 2001-06-01
 ON NUMBER: 09/886342
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100.0%; Score 609; DB 14; Length 117;
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ication US/10006856A
 US20030044841A1
 ION:
 I, Kevin P.
 stein, David

APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan I.
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Fong, Sherman
 APPLICANT: Gao, Wei-Qiang
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, Christopher J.
 APPLICANT: Gurney, Austin L.
 APPLICANT: Hillan, Kenneth J.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nuc
 FILE REFERENCE: P2830P1C14
 CURRENT APPLICATION NUMBER: US/10/006.856A
 CURRENT FILING DATE: 2002-05-10
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 Prior Application removed - See File Wrapper or Palm
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Query Match 100.0%; Score 609; DB 14; Length 117;
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RESULT 9

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 Sequence 9, Application US/10066211
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 GENERAL INFORMATION:
 APPLICANT: Avi J. Ashkenazi
 APPLICANT: Kevin P. Baker
 APPLICANT: David A. Botstein
 APPLICANT: Luc Desnoyers
 APPLICANT: Dan L. Eaton
 APPLICANT: Napoleone Ferrara
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 APPLICANT: Ivar J. Kljavin
 APPLICANT: Jennie P. Mather
 APPLICANT: Mary A. Napier
 APPLICANT: James Pan
 APPLICANT: Nicholas F. Paoni

us-10-066-273-9.rapb

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3	PRIOR FILING DATE: 1999-08-17
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(ON:

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/ E. Gerritsen

cey Goddard

l. J. Godowski

in L. Gurney

r J. Kijavini

ie P. Mather

/ A. Napier

as Pan

olas F. Paoni

aret Ann Roy

thy A. Stewart

iel Tumas

APPLICANT: Colin K. Watanabe
APPLICANT: P. Mickey Williams
APPLICANT: William I. Wood
APPLICANT: Zemin Zang
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUC
FILE REFERENCE: P3130R1C3
CURRENT APPLICATION NUMBER: US/10/066.193
CURRENT FILING DATE: 2002-02-01
PRIOR APPLICATION NUMBER: 10/002.796
PRIOR FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
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PRIOR FILING DATE: 1998-03-25
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PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: 60/149396
PRIOR FILING DATE: 1999-08-17

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; PRIOR APPLICATION NUMBER: 09/886342
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: PCT/US98/14552
; PRIOR FILING DATE: 1998-07-14
; PRIOR APPLICATION NUMBER: PCT/US98/18824
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: PCT/US98/19093
; PRIOR FILING DATE: 1998-09-14
; PRIOR APPLICATION NUMBER: PCT/US98/19330
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; PRIOR FILING DATE: 1998-12-01
; PRIOR APPLICATION NUMBER: PCT/US98/25190
; PRIOR FILING DATE: 1998-11-25
; PRIOR APPLICATION NUMBER: PCT/US99/05028
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: PCT/US99/20111
; PRIOR FILING DATE: 1999-09-01
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547

Query Match 100.0%; Score 609; DB 14; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.7e-58;
Matches 117; Conservative 0; Mismatches 0; Indels 0; GC

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DB 1 MIVGWAFTASRLSGGLLLTLEEHIAHFLGTGGAATTMGNSCICRDDSGTDDSV
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DB 61 QOANSAVPTADTTSRQDPVPRPRGRGPHPRKQKQNVGDLVDTLAVIRTLV

RESULT 11
US-10-006-818A-6
; Sequence 6, Application US/10006818A
; Publication No. US20030054406A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nuc
; FILE REFERENCE: P2830P1C4
; CURRENT APPLICATION NUMBER: US/10/006,818A
; CURRENT FILING DATE: 2001-12-06
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 6
; LENGTH: 117
; TYPE: PRT

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sapiens

peptide

ION: Signal Peptide

feature

4, 32-38, 34-40, 35-41, 51-57

ION: N-Myristoylation Site.

feature

4, 50-54, 113-117

ION: Casein Kinase II Phosphorylation Site.

100.0%; Score 609; DB 14; Length 117;

Identity 100.0%; Pred. No. 1.7e-58; Mismatches 0; Indels 0; Gaps 0;

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ISAVPTADTRSQPRDPVPRPRGRGPHPRKKQNVGDLVLDLTLAVIRTLVDK 117

|||||

Location US/10015393A

IS20030069179A1

ION:

Kevin P.

stein, David

oyers, Luc

on, Dan I.

cara, Napoleone

J, Sherman

Wei-Qiang

iard, Audrey

waki, Paul J.

naldi, Christopher J.

ey, Austin L.

lan, Kenneth J.

James

ti, Nicholas F.

ION: Secreted and Transmembrane Polypeptides and Nucleic

ION: Acids Encoding the Same

P2830P1C46

TION NUMBER: US/10/015.393A

DATE: 2002-06-10

on removed - See File Wrapper or Palm

D NOS: 477

sapiens

peptide

ION: Signal Peptide

feature

4, 32-38, 34-40, 35-41, 51-57

ION: N-Myristoylation Site.

feature

6, 50-54, 113-117

ION: Casein Kinase II Phosphorylation Site.

100.0%; Score 609; DB 14; Length 117;

Best Local Similarity 100.0%; Pred. No. 1.7e-58; Mismatches 117; Conservative 0; Indels 0; G

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Db 1 MIVFGWAVFLASRLGQGLLTLEEHIAHFLGTGGAATTMGNSICRDDSGTDDSV

QY 61 QQAENSAVPTADTRSQPRDPVPRPRGRGPHPRKKQNVGDLVLDLTLAVIRTLVD

Db 61 QQAENSAVPTADTRSQPRDPVPRPRGRGPHPRKKQNVGDLVLDLTLAVIRTLVD

RESULT 13

US-10-015-869A-6

Sequence 6, Application US/10015869A

Publication No. US20030073130A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan I.

APPLICANT: Ferrara, Napoleone

APPLICANT: Fong, Sherman

APPLICANT: Gao, Wei-Qiang

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, Christopher J.

APPLICANT: Gurney, Austin L.

APPLICANT: Hillan, Kenneth J.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nuc

FILE REFERENCE: P2830P1C45

CURRENT APPLICATION NUMBER: US/10/015.869A

Prior Application removed - See File Wrapper or Palm

NUMBER OF SEQ ID NOS: 477

SEQ ID NO 6

LENGTH: 117

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: sig_peptide

LOCATION: 1-16

OTHER INFORMATION: Signal Peptide

FEATURE:

NAME/KEY: misc_feature

LOCATION: 18-24, 32-38, 34-40, 35-41, 51-57

OTHER INFORMATION: N-Myristoylation Site.

FEATURE:

NAME/KEY: misc_feature

LOCATION: 22-26, 50-54, 113-117

OTHER INFORMATION: Casein Kinase II Phosphorylation Site.

US-10-015-869A-6

Query Match

Best Local Similarity 100.0%; Score 609; DB 14; Length 117;

Mismatches 117; Conservative 0; Indels 0; G

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Db 1 MIVFGWAVFLASRLGQGLLTLEEHIAHFLGTGGAATTMGNSICRDDSGTDDSV

QY 61 QQAENSAVPTADTRSQPRDPVPRPRGRGPHPRKKQNVGDLVLDLTLAVIRTLVD

Db 61 QQAENSAVPTADTRSQPRDPVPRPRGRGPHPRKKQNVGDLVLDLTLAVIRTLVD

RESULT 14

US-10-012-121A-6

Sequence 6, Application US/10012121A

Publication No. US20030073810A1

ION: er, Kevin P.
stein, David
snoyers, Luc
on, Dan L.
rara, Napoleone
g, Sherman
o, Wei-Qiang
dard, Audrey
owski, Paul J.
imaldi, Christopher J.
ney, Austin L.
llan, Kenneth J.
n, James
oni, Nicholas F.
TION: Secreted and Transmembrane Polypeptides and Nucleic
Acids Encoding the Same
: P2830PIC20
TION NUMBER: US/10/012.121A
DATE: 2001-12-07
ion removed - See File Wrapper or Palm
ID NOS: 477

o sapiens
peptide
ION: Signal Peptide

c feature
24, 32-38, 34-40, 35-41, 51-57
TION: N-Myristoylation Site.

c feature
26, 50-54, 113-117
TION: Casein Kinase II Phosphorylation Site.

100.0%; Score 609; DB 14; Length 117;
larity 100.0%; Pred. NO. 1.7e-58; Indels 0; Gaps 0;
Conservative 0; Mismatches 0

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lication US/10006116A
US20030082626A1
TION:
er, Kevin P.
stein, David
snoyers, Luc
ton, Dan L.
rara, Napoleone
ng, Sherman
o, Wei-Qiang
dard, Audrey
owski, Paul J.
imaldi, Christopher J.
rney, Austin L.
llan, Kenneth J.
n, James
oni, Nicholas F.
TION: Secreted and Transmembrane Polypeptides and Nucleic

TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2830PIC15
CURRENT APPLICATION NUMBER: US/10/006.116A
CURRENT FILING DATE: 2001-12-16
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PRIOR FILING DATE: 1998-09-01
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TE: 1998-10-28

Query Match 100.0%; Score 609; DB 14; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.7e-58;
Matches 117; Conservative 0; Mismatches 0; Indels 0; G

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Db 1 MIVFGWAVFLASRLGQGLLLTLEEHIAHFLGTGGAATTMGNSCICRDDSSTDSV
Qy 61 QQAENSAVPTADTRSQPRDPVPRRGRGPHPRKKQNVGDLVLTAVIRTLVD
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Search completed: April 2, 2004, 10:28:05
Job time : 41 secs